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                    GenCore version 5.1.6

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OM nucleic - nucleic search, using sw model

Run on:     January 14, 2005, 08:54:47 ; Search time 242.002 Seconds
                                        (without alignments)
                                        8273.863 Million cell updates/sec

Title:          US-09-963-521-1
Perfect score:  2817
Sequence:       1 aatgaaataatccctcacc........tgatctgttccgtcagctgc 2817

Scoring table:  IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched:       824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters:    1649014

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :  Issued Patents NA:*
            1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
            2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

                            SUMMARIES
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Result No.	Score	% Query Match	Match Length	DB	ID	Description
1	2817	100.0	2817	4	US-09-431-099-1	Sequence 1, Appli
2	1836.6	65.2	1909	4	US-09-431-099-3	Sequence 3, Appli
3	1561.6	55.4	1590	4	US-09-602-787A-557	Sequence 557, App
4	157.8	5.6	4403765	3	US-09-103-840A-2	Sequence 2, Appli
5	157.8	5.6	4411529	3	US-09-103-840A-1	Sequence 1, Appli
6	149.4	5.3	36138	4	US-08-311-731A-136	Sequence 136, App
7	72.2	2.6	536165	4	US-09-214-808-1	Sequence 1, Appli
8	71.6	2.5	1446	2	US-08-569-150A-2	Sequence 2, Appli
9	71.6	2.5	2868	3	US-08-274-121B-1	Sequence 1, Appli
10	70.2	2.5	1479	4	US-09-489-039A-7037	Sequence 7037, Ap
11	56	2.0	1455	4	US-09-328-352-595	Sequence 595, App
12	54.6	1.9	2241	4	US-09-248-796A-3169	Sequence 3169, Ap
13	52.6	1.9	3165	4	US-09-614-221A-160	Sequence 160, App
14	48	1.7	654	4	US-09-651-169A-36	Sequence 36, Appl
15	47.6	1.7	7218	1	US-08-232-463-14	Sequence 14, Appl
16	45.8	1.6	1230025	4	US-09-198-452A-1	Sequence 1, Appli
17	45.8	1.6	381	4	US-08-956-171E-4023	Sequence 4023, Ap
18	45.6	1.6	381	4	US-08-781-986A-4023	Sequence 4023, Ap
19	44.8	1.6	400	4	US-08-956-171E-4234	Sequence 4234, Ap
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21	44.8	1.6	3000	1	US-07-841-997A-3	Sequence 3, Appli
22	44.8	1.6	3000	1	US-08-290-301-3	Sequence 3, Appli
23	44.8	1.6	3000	3	US-09-013-598-3	Sequence 3, Appli
24	44.8	1.6	5981	1	US-08-290-301-83	Sequence 83, Appl
25	44.8	1.6	5981	3	US-09-013-598-83	Sequence 83, Appl
c 26	44.6	1.6	4403765	3	US-09-103-840A-2	Sequence 2, Appli
c 27	44.6	1.6	4411529	3	US-09-103-840A-1	Sequence 1, Appli
28	44.4	1.6	237	4	US-08-956-171E-4566	Sequence 4566, Ap
29	44.4	1.6	237	4	US-08-781-986A-4566	Sequence 4566, Ap
30	44.4	1.6	239	4	US-08-956-171E-4543	Sequence 4543, Ap
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32	44.4	1.6	239	4	US-08-956-171E-4544	Sequence 4544, Ap
33	44.4	1.6	239	4	US-08-781-986A-4544	Sequence 4544, Ap
34	44.4	1.6	400	4	US-08-956-171E-3631	Sequence 3631, Ap
35	44.4	1.6	400	4	US-08-956-171E-3660	Sequence 3660, Ap
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38	44.4	1.6	400	4	US-08-781-986A-3660	Sequence 3660, Ap
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40	44.4	1.6	411	4	US-08-956-171E-4353	Sequence 4353, Ap
41	44.4	1.6	411	4	US-08-781-986A-4353	Sequence 4353, Ap
42	44.4	1.6	475	4	US-08-956-171E-3621	Sequence 3621, Ap
43	44.4	1.6	475	4	US-08-781-986A-3621	Sequence 3621, Ap
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                            ALIGNMENTS

RESULT 1
US-09-431-099-1
; Sequence 1, Application US/0941099
; Patent No. 6410705
; GENERAL INFORMATION:
;  APPLICANT: Degussa-Hüls AG
;  APPLICANT: Forschungszentrum-Jülich GmbH
;  TITLE OF INVENTION: New nucleotide sequences coding for the thrE gene and process fo
;  TITLE OF INVENTION: enzymatic production of L-threonine with coryneform bacteria.
;  FILE REFERENCE: 990079 BT
;  CURRENT APPLICATION NUMBER: US/09/431,099
;  CURRENT FILING DATE: 1999-11-01
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: PatentIn Ver. 2.1
;
; SEQ ID NO 1
;  LENGTH: 2817
;  TYPE: DNA
;  ORGANISM: Corynebacterium glutamicum ATCC14752
;  FEATURE:
;  NAME/KEY: CDS
;  LOCATION: (398)..(1864)
;  OTHER INFORMATION: thrE-Gen
US-09-431-099-1

Query Match             100.0%;  Score 2817;  DB 4;  Length 2817;
Best Local Similarity   100.0%;  Pred. No. 0;
Matches 2817; Conservative  0; Mismatches  0; Indels  0; Gaps  0;

Qy    1 AATGAAATAATCCCTCACCAGCCAACTGGCGACATTCAAACACGTTTCATTTCCAAACATCG 60
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Db    1 AATGAAATAATCCCTCACCAGCCAACTGGCGACATTCAAACACGTTTCATTTCCAAACATCG 60

Qy   61 AGCCAAGGGAAAAGAAAGCCCTAAGCCCGTGTTATTAAATGAAGACTCTTTGGAGACC 120
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Db   61 AGCCAAGGGAAAAGAAAGCCCTAAGCCCGTGTTATTAAATGAAGACTCTTTGGAGACC 120

Qy  121 TCAAGCCAAAAGGGGCATTTTCATTAGAAGAAAATACCCCTTTGACCTGGTGTTATTGAGC 180
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Db  121 TCAAGCCAAAAGGGGCATTTTCATTAGAAGAAAATACCCCTTTGACCTGGTGTTATTGAGC 180

Qy  181 TGGAGAAGAGACTTGAACTCTCAACCTACGCATTACAAGTGCGTTGCCTGCCAATTGCG 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 TGGAGAAGAGACTTGAACTCTCAACCTACGCATTACAAGTGCGTTGCCTGCCAATTGCG 240

Qy  241 CCACTCCAGCACCGCAGATGCTGATGATCAACAACTACGAATACGTATCTTAGCGTATGT 300
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241 CCACTCCAGCACCGCAGATGCTGATGATCAACAACTACGAATACGTATCTTAGCGTATGT 300

Qy  301 GTACATCACAATGGAATTCGGGGCTAGAGTATCTGGTGAACGTATCGGCATAAACGACCTGTG 360
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Db  301  GTACATCACAATGGAATCGGGCTAGAGTATCTGGTGAACCGTGCATAAACGACCTGTG  360

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Db  361  ATTGGACTCTTTTTCCTTGCAAAATGTTTTCCAGCGGATTGTGAGTTTTGCGACCCTTCG  420

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Qy  481  GATTGATCTCACTGACCATAGTCAAGTGCCGGTGTGATGAATTGGCTGCGAGAATTGG  540
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Db  481  GATTGATCTCACTGACCATAGTCAAGTGCCGGTGTGATGAATTGGCTGCGAGAATTGG  540

Qy  541  CGATATTTTGCTTTCTTCAGGTACGTCAAACAGTGATGATACCAAGGTGCAAGTTCGAGCGGT  600
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Db  541  CGATATTTTGCTTTCTTCAGGTACGTCAAACAGTGATGATACCAAGGTGCAAGTTCGAGCGGT  600

Qy  601  GACCTCTGCGTGTACTATACGCATGTGAATACGTTGAATACGTTGAATACGTTGAATACGACCAT  660
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Db  601  GACCTCTGCGTGTACTATACGCATGTGAATACGTTGAATACGTTGAATACGTTGAATACGACCAT  660

Qy  661  CTTCACCACAATCGGTGTGGAGGAGATGCCGGTCAACGTGTTTCATGTGTGTGGGCAA  720
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Db  661  CTTCACCACAATCGGTGTGGAGGAGATGCCGGTCAACGTGTTTCATGTGTGTGGGCAA  720

Qy  721  GTTGGACACCAACTTCTCCAAACTGTCTGAGGTTGACCGTTGATCCATTCGACGGC  780
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Db  721  GTTGGACACCAACTTCTCCAAACTGTCTGAGGTTGACCGTTGATCCATTCGACGGC  780

Qy  781  TGGTGCTACCCCGCCTGAGGTTGCGGTTGGCGTTGCTTGGCGCGAGTTGGACGAGCAATCGCCTGC  840
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Qy  841  CTTCACCACAATCGGTGTGGATGGGTGGCGTGGGCGCGCTGTTGCGT  900
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Db  841  CTTCACCACAATCGGTGTGGATGGGTGGCGTGGGCGCGCTGTTGCGT  900

Qy  901  GCTCTTATGGTTTATTGCGTTGCGTTGCCTAATTGCTTTATTGCTTAATTGCTTTTATTACCGCGATCAT  960
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  901  GCTCTTATGGTTTATTGCGTTGCGTTGCCTAATTGCTTTATTGCTTAATTGCTTTTATTACCGCGATCAT  960

Qy  961  TGCCACGACGTCATTTTTGGGAAGAAGAAGGTTTGCCTACTTCTTCCAAAATGTGTTGTTGG  1020
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Db  961  TGCCACGACGTCATTTTTGGGAAGAAGAAGGTTTGCCTACTTCTTCCAAAATGTGTTGTTGG  1020

Qy  1021 TGGTTTATTGCGTTGCGTTGCCTGATTGCGATTGCTTATTCTTTGGCGTTGCAATTTGGTCT  1080
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Db  1021 TGGTTTATTGCGTTGCGTTGCCTGATTGCGATTGCTTATTCTTTGGCGTTGCAATTTGGTCT  1080

Qy  1081 TGAGATCAAACCAGCCAGAATCATCGCATCTGGAATTGTTGTGTGCTGTTGGCAGGTTTGAC  1140
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Db  1081 TGAGATCAAACCAGCCAGAATCATCGCATCTGGAATTGTTGTGTGCTGTTGGCAGGTTTGAC  1140

Qy  1141 ACTTGTGCAATCTCTGAGCAATCGGGCGCATCACGGGGCGCTCCCGTGACGCAGTGCACGATT  1200
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Db  1141 ACTTGTGCAATCTCTGAGCAATCGGGCGCATCACGGGGCGCTCCCGTGACGCAGTGCACGATT  1200

Qy  1201 TTTTGAAACACTTCCTGTTTACCGGCGCATTGTTGCTGCGTGGGTTTGGGCCATTCAGCT  1260
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Db  1201 TTTTGAAACACTTCCTGTTTACCGGCGCATTGTTGCTGCGTGGGTTTGGGCCATTCAGCT  1260

Qy  1261 TTCTGAAATCTTTGCATGTCATGTTGCCATGAGTCCGTGCGACCTAATTATTC  1320
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Qy  1321 GTCTACATTCGCCCGCATTATCGCTGTGTGGCGTCACCCGGCCTTCGCAGTGGGTTG  1380
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Db  1321 GTCTACATTCGCCCGCATTATCGCTGTGTGGCGTCACCCGGCCTTCGCAGTGGGTTG  1380

Qy  1381 TTACGGCGAGTGGTTCCTCGGTGATTATTGCGGGCGCCTTACTCGCGCTGATGGGTTCTGCGTT  1440
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Db  1381 TTACGGCGAGTGGTTCCTCGGTGATTATTGCGGGCGCCTTACTCGCGCTGATGGGTGCGTT  1440
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Qy  1441 TTATTAACCTCTTCGTTGTTGTTATTAGGCCCGTCTCTGCGCGTCTCTGCGCGGATTGCTGCGACCAGC  1500
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Qy  1501 AGTTGGTTCACTGGTGGTTGCTTGCCGCTGCCGTTGCTTCTTGATTCTTGATTCCACCGTTGATTGTGGC  1560
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Db  1501 AGTTGGTTCACTGGTGGTTGCTTGCCGCTGCCGTTGCTTCTTGATTCTTGATTCCACCGTTGATTGTGGC  1560

Qy  1561 GATTGCGCGGCATCACACCAACATTGCGGTTCTAGCAATTTACCGCGGAATGTACGCCAC  1620
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Db  1561 GATTGCGCGGCATCACACCAACATTGCGGTTCTAGCAATTTACCGCGGAATGTACGCCAC  1620

Qy  1621 CTTGAATGATCAAACATTGCGGTTGCTTTAGCCACTGCCTTC  1680
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Qy  1681 ATCACTTGCCGCGTGCTTGTGGGTGGTTTGGGTGAGTGGATTGCCCGCAGGCTACGTCGTCCACC  1740
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Qy  1741 ACGCTTCAACCCATACCGTGCATTTACCAAGGCGAATGAGTTCTCCTTCCAGGAGGAAGC  1800
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Db  1801 TGAGCAGAATCAGCGCGCGCCGAGAGAAACGTCCAAAGACTAATCAAGATTCGGTAATAA  1860

Qy  1861 AAGGTAAAAATCAACCTGCTTAGGGGTCTTTCGCTTAAATAGCGTAGAATATCGGTCGA  1920
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Db  1861 AAGGTAAAAATCAACCTGCTTAGGGGTCTTTCGCTTAAATAGCGTAGAATATCGGTCGA  1920

Qy  1921 TCGCTTTTAAACACTCAGGAGGATCCTTCGGACGCCAAAATCACCGGACACTCGTCGTCCACCC  1980
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Db  1921 TCGCTTTTAAACACTCAGGAGGATCCTTCGGACGCCAAAATCACCGGACACTCGTCCACCC  1980

Qy  1981 CAGAATCCCTTCACGCGTGTTGAACGAGAATTGGTGCCGGATTGTTGTTGCCA  2040
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Qy  2101 AGGGCCTGCGTTACACCAAGGTGCTTCTCGACACGAGAAGCTCAGCGAAGAAGGCTA  2160
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Db  2101 AGGGCCTGCGTTACACCAAGGTGCTTCTCTGAACACGAGAAGCTCAGCGAAGAAGGCTA  2160

Qy  2161 CAAAGCGGACTCGTAAGGCACACCAAGAGAAAACGACCAAGAAGA  2220
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Db  2161 CAAAGCGGACTCGTAAGGCACACCAAGAGAAAACGACCAAGAAGA  2220

Qy  2221 CCACTAAGAAAACTACTAAAAGACCACCGCAAAGAAGAGTCTTAAGCCG  2280
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Qy  2281 GATCTTTATATGGATGATTCCAATAGCTTTGTTGTTGCTCCGCCAGTGGATA  2340
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Qy  2341 TGACTGTCACCGATGTAGCTATAGCATCTCCCCAGCCCCGGTGCCTTGTCACGG  2400
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Qy  2401 GGCTTTCCCGTTCTGGAACATCGTGGATGTTGGGCGGATGGTCGGATCGGAACTGTAG  2460
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Qy  2461 ATGTTGCACCCGACCATTTCGACACAGATACGGGTGTTTGCTGCTCCCCGTGTTGTCCTCA  2520
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Qy  2521 CTGCAAGTGACTATGAAGGCTTCTACGAGGGCTTTCAAACGCAACGCGTGGCCTCTTT 2580
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Db  2521 CTGCAAGTGACTATGAAGGCTTCTACGAGGGCTTTCAAACGCAACGCGTGGCCTCTTT 2580

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Db  2581 TCCACGATTTGATTGTTACTCCGGTGTACACACCGATTGGTGGCATGTGGCTTCGGGAAG 2640

Qy  2641 TAAACCTTCAAGTTCGCTGAAGCCGTGAGCCGTGGGCGGCACACGGTGCCACTGTGTGGG 2700
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Qy  2701 TGCAGGACTATCAGCTGTGTCGGTTCCTGGCATTTGCGCCAGATCGCCCTGATTTGA 2760
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Db  2701 TGCAGGACTATCAGCTGTGTCGGTTCCTGGCATTTGCGCCAGATCGCCCTGATTTGA 2760

Qy  2761 AGATCGTTTCTTCCTCCACATTCCCTTCCCTTCCCTTCCCCTGATCTGTTCCGTCAGCTGC 2817
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Db  2761 AGATCGTTTCTTCCTCCACATTCCCTTCCCTTCCCTTCCCCTGATCTGTTCCGTCAGCTGC 2817
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RESULT 2
US-09-431-099-3
; Sequence 3, Application US/09431099
; Patent No. 6410705
; GENERAL INFORMATION:
; APPLICANT:
; APPLICANT: Forschungszentrum-JOlich GmbH
; APPLICANT: Degussa-HOls AG
; TITLE OF INVENTION: New nucleotide sequences coding for the thrE gene and process fo
; TITLE OF INVENTION: enzymatic production of L-threonine with coryneform bacteria.
; FILE REFERENCE: 990079 BT
; CURRENT APPLICATION NUMBER: US/09/431,099
; CURRENT FILING DATE: 1999-11-01
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 1909
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum ATCC13032
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (280)..(1746)
; OTHER INFORMATION: thrB-Gen
US-09-431-099-3

Query Match 65.2%; Score 1836.6; DB 4; Length 1909;
Best Local Similarity 99.0%; Pred. No. 0;
Matches 1848; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

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Qy   156 CCCCTTTGACCTGGTGTTATTGAGCTGGAGAAGAGACTTGAACTCTCAACCTACGCATTA 215
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Qy   216 CAAGTGCGTTGCGCTGCCAATTGCGCCACTCCAGCACCGCGAGATGCTGATGATCAACAAC 275
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Db    98 CAAGTGCGTTGCGCTGCCAATTGCGCCACTCCAGCACCGCGAGATGCTGATGATCAACAAC 157

Qy   276 TACGAATACGTATCTTAGCGTATGTGTACATCACAAATGGAATTCGGGCGTAGAGTATCTG 335
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Db   218 GTGAACCGTGCATAAACGACCACCTGTGATTGGACTCTTTTCCTTGCAAATGTTTTCCAGC 277

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Qy   516 TGATGAATTGGCTGCGAGAATTGGCGATATTTGCTTTCTTCAGTACGTCAAACAGTG 575
         |||||||||||||||||||||||||||||||||||||||||||||||||||| ||||
Db   398 TGATGAATTGGCTGCGAGAATTGGCGATATTTGCTTTCTTCAGTACGTCAAATAGTG 457

Qy   576 ATACCAAGTGCAAGTTCGAGCCGTGACCTCGTGCTTCGGCATGTGG 635
         | |||||| ||||||||||| ||||||||||||||
Db   458 ACACCAAGTACAAGTTCGAGCAGTGACCTCGTGCTTGTACTACACGCACGTGG 517

Qy   636 ATATCACGTTGAATACGATCACCACATCTTCACCACACCGGTGTGGAGAGGAGATGCCGG 695
         ||||||||||||||||||||||||||||||||||||| |||||||||||||| |||||||
Db   518 ATATCACGTTGAATACGATCACCACATCTTCACCACATCCGGTGTGGAGAGGAAGATGCCGG 577

Qy   696 TCAACGTGTTCATGTTGTGGGCAAGTTGGACACCAACTTCTCCAAACTGTCTGAGGTTG 755
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   578 TCAACGTGTTCATGTTGTGGGCAAGTTGGACACCAACTTCTCCAAACTGTCTGAGGTTG 637

Qy   756 ACCGTTTGATCCGTTCCATTCAGGCTGGTGGTCTACCCCGCTGGTGCCGACCCTGGCTGGG 815
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   638 ACCGTTTGATCCGTTCCATTCAGGCTGGTGGTCCCCGCGACCCTGGCTGGG 697

Qy   816 TGGACGAGTGGAGCAATCGCCGCGTCCTATCGTTCCCGTGTTCCCGTGCTTGGCTCTGGG 875
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Db   698 TGGACGAGTGGAGCAATCGCCGCGTCCTATCGTTCCCGTGTTCCCGTGCTTGGCTCTGGG 757

Qy   876 CAATGATGGTGGCCGCTGTGCTGTCGTGCTGTCGTGGGTGGGGTGGATGGCAGGTTTCCCTAATTG 935
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   758 CAATGATGGGGTGGTGCTGTCGTGCTGTCGTGGGTGGGGTGGATGGCAGGTTTCCCTAATTG 817

Qy   936 CTTTTATTACCGGGTTCACGACTTCACGACGTCATTTTTGGGAAAGAAGGGTTGC 995
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   818 CTTTTATTACCGCGTTCACGATCATTGCCACGACGTCATTTTTGGGAAAGAAGGGTTGC 877

Qy   996 CTACTTTCTTCCAAAATGTTGGTGGGTTTATTGGCCACGCTGCCTGCGTCGATTGCTT 1055
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   878 CTACTTTCTTCCAAAATGTTGGTGGGTTTATTGCCACGCTGCCTGCGTCGATTGCTT 937

Qy  1056 ATTCTTTGGCGTTGCAATTGGTCTTGAGATCAAACCGAGCCAGATCATCGCATCTGGAA 1115
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   938 ATTCTTTGGCGTTGCAATTGGTCTTGAGATCAAACCGAGCCAGATCATCGCATCTGGAA 997

Qy  1116 TTGTTGTGCTGTTGGCAGTTGGACACTTGTCAATCTGTGCCATCACAGGGACGG 1175
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   998 TTGTTGTGCTGTTGGCAGTTGGACACTTGTCAATCTGTGCCATCACAGGGACGG 1057

Qy  1176 CTCCGGTGACAGCAAGTGCACGATTTTTGAAACACTCCTGTTTACCGGCGGCATTGTTG 1235
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1058 CTCCGGTGACAGCAAGTGCACGATTTTTCGAAACACTCCTGTTTACCGGCGGCATTGTTG 1117

Qy  1236 CTGGCGTGGGTTGGGCATTCAGCTTTCGAAATCTTCGAAATCTTCGATGTTCGCATGTTGCCTGCCATGG 1295
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1118 CTGGCGTGGGTTGGGCATTCAGCTTTCGAAATCTTCGAAATCTTCGATGTTCGCATGTTGCCTGCCATGG 1177

Qy  1296 AGTCCGCTGCAGCACCTAATTATTCGTCTACATTGCGCTGGTGTGGCGTCA 1355
         ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1178 AGTCCGCTGCAGCACCTAATTATTCGTCTACATTGCGCTGGTGTGGCGTCA 1237

Qy  1356 CCGCAGCGGCCTTCGCAGTGGGTGTTGTTACGCGGAGTGGTCCTCGGGAATTGCGGGGC 1415
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1238 CCGCAGCGGCCTTCGCAGTGGGTGTTGTTACGCGGAGTGGTCCTCGGGAATTGCGGGGC 1297

Qy  1416 TTACTGCCTGATGGGTTCGCGTTTATTGTTATTACCTTCGTGTTATTTAGGCCCCGTCT 1475
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1298 TTACTGCCTGATGGGTTCGCGATTGGTTCGCGTTGTTGTTATTACCTTCGTGTTATTTAGGCCCCGTCT 1357

Qy  1476 CTGCCGCTGCGATTGCTGCAACAGCAGTGGTTTCACTGGTTTGCTTGCCCGTCGAT 1535
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1358 CTGCCGCTGCGATTGCTGCAACAGCAGTGGTTTCACTGGTTTGCTTGCCCGTCGAT 1417

Qy  1536 TCTTGATTCCACCGTTGCACCGGCCATCAGACCATCACAACACTCCAGGTCTAG 1595
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1418 TCTTGATTCCACCGTTGCACCGGCCATCAGACCATCACAACACTCCAGGTCTAG 1477

Qy  1596 CAATTTACCGCGGAATGTACGCCACCTTGAATGATCAAACACTCATGGGTTTCACCAACA 1655
Db
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Db   1478 CAATTTACCGCGGAATGTAGCCACCTGCTTCATCACTTGCCGCTGGTCAAACACTCATGGGTTTCACCAACA 1537
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Qy   1656 TTGCCGGTTGCTTAGCCACTGCTTCATCACTTGCCGCTGGTCGTGCGTGTTTTGGGTCAGTGGA 1715
          ||||||||||||||||||||||||||||||||||||||||||||||||
Db   1538 TTGCCGGTTGCTTAGCCACTGCTTCATCACTTGCCGCTGGTCGTGCGTGTTTTGGGTCAGTGGA 1597
Qy   1716 TTGCCCGCAGGCTACGTCGTCCACCACGCTTCAACCCATACCGTGCATTTACCAAGGCGGA 1775
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1598 TTGCCCGCAGGCTACGTCGTCCACCACGCTTCAACCCATACCGTGCATTTACCAAGGCGGA 1657
Qy   1776 ATGAGTTCTCCTTCCAGGAGGAAGCTGAGCGAGAATCAGCGCCGGCGAGAGAAACGTCCAA 1835
          |||||||||||||||||||||||||||||||||||||||||
Db   1658 ATGAGTTCTCCTTCCAGGAGGAAGCTGAGCGAGAATCAGCGCCGGCAGAAAACGTCCAA 1717
Qy   1836 AGACTAATCAAAGATTCGGTAATAAAAGTAAAAATCAACCTGCTTAGGCGTCTTCGCT 1895
          ||| |||||||||||||||||||||||||||||||||||||||||||
Db   1718 AGACTAATCAGAGATTCGGTAATAAAAGTAAAAATCAACCTGCTTAGGCGTCTTCGCT 1777
Qy   1896 TAAATAGCGTAGAATATCGGGTCGATCGTTTTAAACACTCAGGAGGATCCTTGCCGCC 1955
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db   1778 TAAATAGCGTAGAATATCGGGTCGATCGTTTTAAACACTCAGGAGGATCCTTGCCCGCC 1837
Qy   1956 AAAATCACCGACACTCGTCCACCCAGAATCCCTTCACGCGTGTTGAAGAGGAAACCCGCA 2015
          |||||||||||||||||||||||||||||||||||||||||||||
Db   1838 AAAATCACCGACACTCGTCCACCCAGAATCCCTTCACGCGTGTTGAAGAGGAAACCCGCA 1897
Qy   2016 GCCCGGTG 2022
          ||||||| |
Db   1898 GCCCGGGG 1904
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RESULT 3
US-09-602-787A-557

; Sequence 557, Application US/09602787A
; Patent No. 6696561
; GENERAL INFORMATION:
; APPLICANT: Pompejus, Mark
; APPLICANT: Kr"ger, Burkhard
; APPLICANT: Sch"der, Hartwig
; APPLICANT: Zelder, Oskar
; APPLICANT: Haberhauer, Gregor
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS
; TITLE OF INVENTION: INVOLVED IN MEMBRANE SYNTHESIS AND MEMBRANE
; TITLE OF INVENTION: TRANSPORT
; FILE REFERENCE: BGI-125CP
; CURRENT APPLICATION NUMBER: US/09/602,787A
; CURRENT FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: USSN 60/141031
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: DE 19931454.3
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931478.0
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931563.9
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19932122.1
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932124.8
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932125.6
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932128.0
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932180.9
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932182.5
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932190.6
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932191.4
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932209.0
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932212.0
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932227.9
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932228.7
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; PRIOR APPLICATION NUMBER: DE 19932229.5
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932230.9
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932927.3
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: DE 19933005.0
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: DE 19933006.9
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: DE 19940764.9
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: DE 19940765.7
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: DE 19940766.5
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: DE 19940830.0
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: DE 19940831.9
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: DE 19940832.7
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: DE 19940833.5
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: DE 19941378.9
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: DE 19941379.7
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: DE 19941395.9
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: DE 19942077.7
; PRIOR FILING DATE: 1999-09-03
; PRIOR APPLICATION NUMBER: DE 19942078.5
; PRIOR FILING DATE: 1999-09-03
; PRIOR APPLICATION NUMBER: DE 19942079.3
; PRIOR FILING DATE: 1999-09-03
; PRIOR APPLICATION NUMBER: DE 19942088.2
; PRIOR FILING DATE: 1999-09-03
; NUMBER OF SEQ ID NOS: 678
; SEQ ID NO 557
; LENGTH: 1590
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (101)..(1567)
; OTHER INFORMATION: RXN00349
US-09-602-787A-557

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Query Match         55.4%;  Score 1561.2;  DB 4;  Length 1590;
Best Local Similarity  98.9%;  Pred. No. 0;
Matches 1572;  Conservative  0;  Mismatches 18;  Indels  0;  Gaps  0;

Qy   298 TGTGTACATCACAATGGAATTCGGGCGCTAGAGTATCTGGTGAACCGTGCATAAACGACCT 357
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1 TGTGTACATCACAATGGAATTCGGGCGCTAGAGTATCTGGTGAACCGTGCATAAACGACCT 60
Qy   358 GTGATTGGACTCTTTTCCTTGCAAAATGTTTTCCAGCGGATGTTGAGTTTTCGCACCCT 417
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61 GTGATTGGACTCTTTTCCTTGCAAAATGTTTTCCAGCGGATGTTGAGTTTTCGCACCCT 120
Qy   418 TCGTGGCCGCATTCAACAGTTGACGCTGCAAAAGCCGCACCTCCGCCATCGCCACTAGC 477
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 TCGTGGCCGCATTCAACAGTTGACGCTGCAAAAGCCGCACCTCCGCCATCGCCACTAGC 180
Qy   478 CCCGATTGATCTCACTGACCATAGTCAAGTGCCGGTGTGATGAATTTGGCTGCGAGAAT 537
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         CCCGATTGATCTCACTGACACCAATGTCCGGGTGTGAGAATTTGGCTGCGAGAAT 240

Qy   538 TGGCGATATTTGCTTCTTCAGGTACGTCAAACAGTGACGTGATACCAAGGTCGAAGTTCGAGC 597
         |||||| ||||| |||||||||||||||||||| ||||||||||||||||||||||||
Db   241 TGGCGATATTTGCTTCTTCAGGTACGTCAAATAGTGACACCAAGGTACAAGTTCGAGC 300

Qy   598 GGTGACCCTCTGCCTATGCCTGTACTATACGGTTGTACTACACGACGTGGATATCGGTTGAATACGATCAC 657
         |||||||||||||||||||||||||||||||| |||||||||||||||||||||||||||
Db   301 AGTGACCTTCGGCGTACGGTTGTACTACACGACGTGGATATCACGTTGAATACGATCAC 360

Qy   658 CATCTTCACCACACATCGGTGTGGAGAGAAGATGCCGGTCAACGTGTTTCATGTTGTTGGG 717
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 CATCTTCACCACACATCGGTGTGGAGAGAAGATGCCGGTCAACGTGTTTCATGTTGTAGG 420

Qy   718 CAAGTTGGACACCAACTTCTCAAACTGTCTGAGGTTGACCGTTGATCCGTTCCATTCA 777
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 CAAGTTGGACACCAACTTCTCAAACTGTCTGAGGTTGACCGTTGATCCGTTCCATTCA 480

Qy   778 GGCTGGTGCTACCCGCGCTGAGGTTGCCGAGAAATTCTGGACGAGTTGGAGCAATCGCC 837
         ||||||||||||||||||||||||||||||||| |||||||||||||||||||||||||
Db   481 GGCTGGTGCGACCCGCGCTGAGGTTGCCGAGAAATCCTGGACGAGTTGGAGCAATCCCC 540

Qy   838 TGGCGTCTTATGGTTCCCGTGTTGCGTTGCGTTGCTTGGGCAATGATGAGGTGGCGCTGTTGC 897
         |||||||||||||||||||||||||||||||||||| |||||||||||||||||||||||
Db   541 TGCGTCTTATGGTTTCGTTGCGTTGCGTTGCGTTGGGCAATGATGGGTGGTGCTGTTGC 600

Qy   898 TGTGCTGTTGGGGTGGTGGATGGCAGGTTCCCTAATTGCTTTTATTACCGCGTTCACGAT 957
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601 TGTGCTGTTGGGGTGGTGGATGGCAGGTTCCCTAATTGCTTTTATTACCGCGTTCACGAT 660

Qy   958 CATTGCCACGACGTCATTTTTGGGAAAGAAGGGTTTGCCTACTTTCTTCCAAAATGTTGT 1017
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   661 CATTGCCACGACGTCATTTTTGGGAAAGAAGGGTTTGCCTACTTTCTTCCAAAATGTTGT 720

Qy  1018 TGGTGGTTTATTGCCACGCTGCCTGCGATTGCTTATTCTTCGGCGTTGCAATTTGG 1077
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Db   721 TGGTGGTTTATTGCCACGCTGCCTGCGATTGCTTATTCTTTGGCGTTGCAATTTGG 780

Qy  1078 TCTTGAGATCAAACCGAGCCAGATCATCGCTCGGAATTGTTGTGCTTGGCAGTTT 1137
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   781 TCTTGAGATCAAACCGAGCCAGATCATCGCTCGGAATTGTTGTGCTTGGCAGTTT 840

Qy  1138 GACACTTGTGCAATCTCTGCAGGACGACGCATCACGGGCGCTCCGGTGACAGTGCACG 1197
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   841 GACACTCGTGCAATCTCTGCAGGACGACGCATCACGGGCGCTCCGGTGACAGTGCACG 900

Qy  1198 ATTTTTGAAACACTCCGTTTACCGGCGCAATTGTTGCGGGGCATTGTTTGGGCATTCA 1257
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Db   901 ATTTTTCGAAACACTCCGTTTACCGGCGCAATTGTTGCGGGGCATTGTTTGGGCATTCA 960

Qy  1258 GCTTTCTGAAATCTGCATGTGCCTGCGCATGTGCCTGCGCATGGAGTCCGGTCAGCACCTAATTA 1317
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Db   961 GCTTTCTGAAATCTGCATGTGCCTGCGCATGTGCCTGCGCATGGAGTCCGGTCAGCACCTAATTA 1020

Qy  1318 TTCGTCTACATTCGCCCGCCATTATCGCGTGGTGGCGTCACCGGCCTTCGCAGTTGGG 1377
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1021 TTCGTCTACATTCGCCCGCCATTATCGCGTGGTGGCGTCACCGGCCTTCGCAGTTGGG 1080

Qy  1378 TTGTTTACGCGGAGTGGTCCTCGGCGGTCTTCTCGGCGGCTTACTGCGCTGATGGGTTCTGC 1437
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1081 TTGTTTACGCGGAGTGGTCCTCGGCGGTCTTCTCGGCGGCTTACTGCGCTGATGGGTTCTGC 1140

Qy  1438 GTTTATTACCTCTTCGTTGTTGTTTATTAGCCCCGTCTCTGCGCGGATTGCTGCAAC 1497
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Db  1141 GTTTATTACCTCTTCGTTGTTGTTTATTAGCCCCGTCTCTGCGCGGATTGCTGCAAC 1200

Qy  1498 AGCAGTTGGTTTCACTGGTGGTTTGCTTGCCCCGTCGATTCTTGATTCCACCGTTGATTGT 1557
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Db  1201 AGCAGTTGGTTTCACTGGTGGTTTGCTTGCCCCGTCGATTCTTGATTCCACCGTTGATTGT 1260

Qy  1558 GGCGGATTGCCGGCATCACCAATGCTTCCAGGTCTAGCAATTACCGCGGAATGTACGC 1617
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Db  1261 GGCGGATTGCCGGCATCACCAATGCTTCCAGGTCTAGCAATTACCGCGGAATGTACGC 1320

Qy  1618 CACCTTGAATGATCAAACACTCATGGGTTTCACCAACATGCGGTGCTTTAGCCACTGC 1677
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Db  1321 CACCCTGAATGATCAAACACTCATGGGTTTCACCAACATTGCGGTGCTTTAGCCACTGC 1380

Qy  1678 TTCATCACTTGCCTGCCGTGGTGGTGTTTGGTGGTGAGTGAGGTCACGCTACGTCGTCC 1737
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Db  1381 TTCATCACTTGCCTGCCGTGGTGGTGTTTGGTGGTGAGTGAGGTCACGTCGTCGTCC 1440

Qy  1738 ACCACGCTTCAACCCATACCGTGCATTACCAAGGCGAATGAGTCTCCTTCCAGGAGGA 1797
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Db  1441 ACCACGCTTCAACCCATACCGTGCATTACCAAGGCGAATGAGTCTCCTTCCAGGAGGA 1500

Qy  1798 AGCTGAGCAGAATCAGCCGCCGGCCAGAGAGAAACGTCCAAAGACTAATCAAAGATTCGGTAA 1857
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Db  1501 AGCTGAGCAGAATCAGCCGCCGGCCAGAGAGAAACGTCCAAAGACTAATCAGAGATTCGGTAA 1560

Qy  1858 TAAAAGGTAAAAAATCAACCTGCTTAGGCGT 1887
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Db  1561 TAAAAGGTAAAAAATCAACCTGCTTAGGCGT 1590
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RESULT 4
US-09-103-840A-2

; Sequence 2, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
;   APPLICANT: FLEISCHMAN, Robert D.
;   APPLICANT: WHITE, Owen R.
;   APPLICANT: FRASER, Claire M.
;   APPLICANT: VENTER, John C.
;   TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
;   TITLE OF INVENTION: TUBERCULOSIS
;   FILE REFERENCE: 24366-20007.00
;   CURRENT APPLICATION NUMBER: US/09/103,840A
;   CURRENT FILING DATE: 1998-06-24
;   NUMBER OF SEQ ID NOS: 2
;   SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
;   LENGTH: 4403765
;   TYPE: DNA
;   ORGANISM: Mycobacterium tuberculosis
; FEATURE:
;   OTHER INFORMATION: CDC 1551
;   OTHER INFORMATION: "n" bases at various positions throughout the sequence
;   OTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2

Query Match   5.6%; Score 157.8; DB 3; Length 4403765;
Best Local Similarity   58.2%; Pred. No. 2.1e-38;
Matches 310; Conservative   0; Mismatches 202; Indels 21; Gaps 1;

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Qy  2306 CTTTGTAGTTGTTGCTAACCGTCTGCTAACCGTGGATATGACTGCCAGATGAGTAGTCA 2365
         |||||||||||||||||| |||||||||||||||||||||||||||||||||||||||
Db 3902073 CTTTGTAGTTGGTAGCCAATCGACTGCCCGTCGATCTCGGAGCGTCTTCCCGACGGCAGCAC 3902132

Qy  2366 TAGCATCTCCCCAGCCCCGGCCTTGTGCCCGGAGCGCCCGGAGGGTTGGGGCCGGCGTCG 2425
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3902133 AACCTGGAAACGCAGCAGCCCCGGAGGCTTCCCGGTTCTGGAGCCGGTGCTGCGGCGGTCG 3902192

Qy  2426 TCGTTGGATGTTGGGGTCGGATGAGTGCCTGGAACTGTCACCCGAACCATTGCAAC 2485
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3902193 GCGCCGGGCGCTGGGTCGGCGGCTCGGCCGGCCGTAACGACACGGGGCCGAACCTCCA 3902252

Qy  2486 AGATACGGGTG--------------TTTTGCTGCACCGTGTCCTCACTGC 2524
         ||||||||||              ||||||||||||||||||||||||||
Db 3902253 CGTGCTGGACGGCCCCATCATCCAAGACGAGCTGGAACTTCATCCGTACGGCTGAGCAC 3902312

Qy  2525 AAGTGACTATGAAGGCTTCTACGAGGGCTTTTCAAACGCAACGAACTGTGGGCCTCTTTTCCA 2584
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3902313 CACGGACGACGTAGCTCAGTAGTACGACGGGGATTCTCCAACGCCACACTGTGGCCGCTGTACCA 3902372
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Qy  2585 CGATTTGATTGTTACTCCGGTGTACACACCGATTGGTGCGCATGCGTTCGGGAAGTAAA 2644
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Db 3902373 CGACGTCATCGTCAAGCCGCTCTACCACCGGAATGCTGGGATCGCTCGACGTCA 3902432
Qy  2645 CCTCAAGTTCGCTGAGCCGTGAGCCAAGTGGCGGCACACGGTGCCACTGTGTGGGTGCA 2704
Db 3902433 CCAGCGCTTGCGAGGCGGCGCGCCGCCCAACGGCGCAACCGTGTGGGTACA 3902492
Qy  2705 GGACTATCAGCTGTTCGTGCTCGGTTCCTGGCCATTTGCGCCAGATGCGCCCTGATTTGAAGAT 2764
Db 3902493 GGACTACCAGCTGCAGCTGGTACCGAAGATGCTGCGGCCCGATCTGACCAT 3902552
Qy  2765 CGGTTTCTTCTTCCCACATTCCCTTCCCGTTCCCGTCGTCCGTCAGCTGC 2817
Db 3902553 CGGTTTCTTTTTGCACATCCCGTTCCCGCCGGTAGAGAGCTGTTTATGCAGATGC 3902605
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RESULT 5
US-09-103-840A-1
; Sequence 1, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; TITLE OF INVENTION: TUBERCULOSIS
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 4411529
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; OTHER INFORMATION: H37Rv
US-09-103-840A-1

Query Match   5.6%; Score 157.8; DB 3; Length 4411529;
Best Local Similarity 58.2%; Pred. No. 2.1e-38;
Matches 310; Conservative 0; Mismatches 202; Indels 21; Gaps 1;

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Qy  2306 CTTTGTAGTTGTTGCTAACCGTCTGCCAGTGGATATGCATCGTCCACCCAGATGGTAGCTA 2365
Db 3908294 CTTCGTGTGGTGGTAGTAGCCAATCGACTGCCCGTATCGAGCCGTCTTCCCGACACGGCAC 3908353
Qy  2366 TAGCATCTCCCCCAGCCCCGGTGCCTTTGTCACGGGCCTTTCCCCGGTTCTGGAACAACA 2425
Db 3908354 AACCTGGAAAACGCAGCCCCGGAGCTTGGTCACGGCCCTTGCGCTGTCGCGGGGCGTCG 3908413
Qy  2426 TCGTGGATGTTGGGTCGGATGGCCTGAACTGTTGCACCCGAACCATTTCGAAC 2485
Db 3908414 GCGCGGGGCCTGGGTCGGCGTGCCGCGGGGCCGAACCCGACCTCCA 3908473
Qy  2486 AGATACGGGTG--------------TTTTGCTGCACCCTGTGTCCTTGTCCTCACTGC 2524
Db 3908474 CGTGCTGACGCGACGGCCCCATCATCCAAGACGAGCTGGAACTTCATCCCGTACGGCTGAGCAC 3908533
Qy  2525 AAGTGACTATGAAGGCTTCTACGAGGCCTTTCAAACGCAACGCGTGTGGGCCTCTTTTCCA 2584
Db 3908534 CACGGACGAATAGCTCAGTACTACGAGGAATTCTCCAACGCCACACTGTGGGCCGCTGTACCA 3908593
Qy  2585 CGATTTGATTGTTACTCCGGTGTACACACCGATTGGTGCGCATGCGTTCGGGAAGTAAA 2644
Db 3908594 CGACGTCATCGTCAAGCCGCTCTACCACCGGAATGCTGGGATCGCTCGACGTCA 3908653
Qy  2645 CCTCAAGTTCGCTGAGCCGTGAGCCAAGTGGCGGCACACGGTGCCACTGTGTGGGTGCA 2704
Db 3908654 CCAGCGCTTGCGAGGCGGCGCGCCGCCCAACGGCGCAACCGTGTGGGTACA 3908713
Qy  2705 GGACTATCAGCTGTTCGTGCTCGGTTCCTGGCCATTTGCGCCAGATGCGCCCTGATTTGAAGAT 2764
```

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Db 3908714 GGACTACCAGCTGCAGCTGGTACCGAAGATGCTGCGGCCCGATCTGACCAT 3908773
Qy  2765 CGGTTTCTTCTTCCCACATTCCCTTCCCGTTCCCGTCGTCCGTCAGCTGC 2817
Db 3908774 CGGTTTCTTTTTGCACATCCCGTTCCCGCCGGTAGAGAGCTGTTTATGCAGATGC 3908826
```

RESULT 6
US-08-311-731A-136
; Sequence 136, Application US/08311731A
; Patent No. 658266
; GENERAL INFORMATION:
; APPLICANT: SMITH, DOUGLAS
; APPLICANT: MAO, JEN-I
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
; TITLE OF INVENTION: RELATING TO MYCOBACTERIUM TUBERCULOSIS AND LAPRAE FOR
; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 411
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: WOLF, GREENFIELD & SACKS, P.C.
; STREET: 600 ATLANTIC AVENUE
; CITY: BOSTON
; STATE: MASSACHUSETTS
; COUNTRY: USA
; ZIP: 02210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/311,731A
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: GATES, EDWARD R.
; REGISTRATION NUMBER: 31,616
; REFERENCE/DOCKET NUMBER: C0044/7125
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/720-3500
; TELEFAX: 617/720-2441
; INFORMATION FOR SEQ ID NO: 136:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 36138 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Mycobacterium leprae
US-08-311-731A-136

Query Match   5.3%; Score 149.4; DB 4; Length 36138;
Best Local Similarity 57.1%; Pred. No. 2.7e-37;
Matches 301; Conservative 0; Mismatches 211; Indels 15; Gaps 1;

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Qy  2306 CTTTGTAGTTGTTGCTAACCGTCTGCCAGTGGATATGCATCGTCCACCCAGATGGTAGCTA 2365
Db 27896 CTTCGTGTAGTTGGTGGTCGCCAATCGACGTCGATCCAGGTGCCACTGC 27955
Qy  2366 TAGCATCTCCCCCAGCCCCGGTGCCTTTGTCACGGGCCTTTCCCCGGTTCTGGAACAACA 2425
Db 27956 GATCTGGAAGCGCAGTCCAGCGGGTTGGTCAGCGGGGCCGCGTGCTGCGTCGGTCAGCG 28015
Qy  2426 TCGTGGATGTTGGGTCGGATGGCCTGAACTGTTGCACCCGAACCATTTCGAAC 2485
Db 28016 GCGCGGGGCCTGGGTCGGCGTGCCGCGGGCGTAATAAACGACAACGTGGACCTGCGACTTGAC 28075
Qy  2486 AGATACG--------------GGTGTTTTGCTGCACCGTGTGTCCTCACTGCAAGTGA 2530
```

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Db    28076 CATCAAGTCGATCGTGCGAGGATGGCCTTACTCTTTATCCGGTACGGCTGAACACACATGA 28135
                                                                             |
Db          317698 C 317698

Qy     2531 CTATGAAGGCTTCTACGAGGGCTTTTCAAACGCAACGCGTGGGCTCTTTCCACGATTT 2590
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    28136 TGTCGCCGAGTACTACGAGGGGTTCTCGAACGCCACGCGTGTGGCCGCTATACCACGACGT 28195

Qy     2591 GATTGTTACTCCGGTGTACAACACCGATTGGTGCATGCGTTTCGGGAAGTAAACCTCAA 2650
            |||||||| |||  || ||||||||||||||||||||| ||||||||||||||||||
Db    28196 CATCGTAAGCCCATTTACCACTGCGAATGGTGGGAACGCTACGTCGATGTCAACCGGCG 28255

Qy     2651 GTTCGCTGAAGCCGTGAGCCAAGTGCGGCACACGGTGCCACTGTGTGGGTGCAGGACTA 2710
            |||||||| ||||||| |||||||||||||||||||||||||||||||||||||||||
Db    28256 CTTCGCCGAAACAACGTCACGCACAGCCGCCTACGGTGGGACCGTATGGGTGCAGGACTA 28315

Qy     2711 TCAGCTGTGTGCTGGTTCCTGGCATTTGCGCCAGATGCGCCCTGATTTGAAGATCGGTTT 2770
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    28316 CCAACTGCAATTGGTACCGAAGATGCTGCGCATAATGCGGCCCGACTTGACCATCGGTTT 28375

Qy     2771 CTTCCTCCACATTCCCTTCCCTTCCCGATCTGTTCCGTCAGCTGC 2817
            |||||   |||||| | |||| |||||||||||  |||  |||  |||
Db    28376 CTTCTTGCACATCCCGTTCCCGCCGGTCCCGCCGGTGGAGCTGTGTTCATGCAGATAC 28422
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Query Match            2.6%;    Score 72.2;  DB 4;  Length 536165;
Best Local Similarity  52.5%;   Pred. No. 1.1e-10;
Matches  158;  Conservative    0;  Mismatches 143;  Indels    0;  Gaps    0;

Qy     2517 CTCACTGCAAGTGACTATGAAGGCTTCTACGAGGGCTTTCAAACGCAACGCGTGTGGCCT 2576
            |||||||||||||||||||||||||||||||||||||  |||||||||||||||||
Db   317398 CTGACCGATACCGACGTAGAGGAATACTACCACGCGGCTTCGCCACCGCGGTTCTCTGGCCG 317457

Qy     2577 CTTTTCCACGACGATTTGATTGTTACTCCGGTGTACAACACCGATTGGTGCATGCGTTTCGG 2636
            ||||| ||||||||||||||||| |||||||||||||||  |||||||||||||
Db   317458 ATTTGCCACTACCGCCTTGATCTCGCCGAATACGGTCGCAAGGAAATGGCCGGGTATTTC 317517

Qy     2637 GAAGTAAACCTCAAGTTCGCTGAAGCCGTGAGCCGCGCCTGGAGCCGCGCCATCGTG 2696
            |||||||||||||||| ||||||||||| || | | |||||||| ||||| ||||||
Db   317518 CGCGTCAACCGCGTTCTTCGCCACCATCGACCCGGCCCGCTGTGTCAAACCCGATGACGTCATT 317577

Qy     2697 TGGGTGCAGGACTATCAGCTGTTGCTGGTTCCTGGCATTTTGCGCCAGATCGCGCCCTGAT 2756
            |||||||||||||||||| |||||||||||||| |||| |||||||  | ||||| |||
Db   317578 TGGGTGCACGACTACCCCGTGATTCCTCGCGCCGGGAACTGCGTCAGATGGGCGCCTGGAG 317637

Qy     2757 TTGAAGATCGGTTTCTTCCTCCACATTCCCTTCCCTTCCCGATCTGTTCCGTCAGCTG 2816
            |||||||||| |||||| ||||| ||||| | ||||||||||||||||
Db   317638 AACCGCATCGGGCTTCTTCCTCCACATTCCCACATTCCCTGCGCCGCTGCGACGTACTCTTCACGATG 317697

Qy     2817 C 2817
            |
Db   317697 C 317697
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Query Match            2.5%;    Score 71.6;  DB 2;  Length 1446;
Best Local Similarity  49.1%;   Pred. No. 1.4e-12;
Matches  222;  Conservative    0;  Mismatches 224;  Indels    6;  Gaps    1;

Qy     2372 CTCCCCAGCCCCGTGGCCTTGTCACGGGGCTTTCCCCGTTCTGGAACAACATCGTGG 2431
            ||||| |||||| || |||||| | |||  |||||||| |||||
Db       75 CGCCGGCCAGTGCCGGTGGCCTTCGCCGTTGGCATACTGGGGCGCACTGGGGCACTCCGGTGG 134

Qy     2432 ATGTTGGGTCGGATGGCCTGGAACTGTAGATGTTGCACCCGAACCATTTCGAACAGATAC 2491
            ||||  ||| |||| ||||| |||| | |||| || ||| |||||
Db      135 ACTGTGGGTTTGGCTGGAGTCGGTGAAACAGGGAATGAGGAATGAGGGAATGAGGTGAA 194
```

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;    TOPOLOGY: linear
;    MOLECULE TYPE: genomic DNA
US-08-274-121B-1

Query Match         2.5%;    Score 71.6;    DB 3;    Length 2868;
Best Local Similarity   49.1%;    Pred. No. 2.4e-12;
Matches 222;    Conservative 0;    Mismatches 224;    Indels 6;    Gaps 1;

Qy    2372  CTCCCCAGCCCGTGGCCTTGTCACGGGCGCTTCCCCGTCTCGAACAACATCGTG  2431
            |||||||||||||||||||||||||||||||||||||||||||||||||
Db    1500  CGCCCCAGTGCCGTGGCCTTGCCGTTGCATACTGGGGCACTGAAAGCCGCAGGCGG  1559

Qy    2432  ATGTTGGGTCGGATGGCCTGGAACTGTAGATGTTGCACCGGAACCATTTGAACAGATAC  2491
            |||||||||||||||||||||||||||||||||||||||||
Db    1560  ACTGTGGTTTGGGTCGGAGTGGTGAAACAGGGAATGAGGATCAGCCGCTAAAAAAGGTGAA  1619

Qy    2492  GGGTG------TTTTGCTGCGCACCCTGTTGTCCTCACTGCAAGTGACTATGAAGGGCTTCTA  2545
            ||||                   |||||||||||||||||||||||||
Db    1620  AAAAGGTAACATTACGTCGGCCTCTTTTAACCTCAGCGAACAGGACCTTGACGAATACTA  1679

Qy    2546  CGAGGGCTTTCAAACGCAACGGTGTGGCCCTCTTTTTCCACGATTTGATTGTTACTCCGGT  2605
            ||||||||||||||||||||||||||||||||||||||||
Db    1680  CAACCAATTCTCCAATGCCGTTCTCTCGGCCCCGGCCTTTCATTATCGGGCTTCGGTGGTGCA  1739

Qy    2606  GTACAAACACCGATTGGTGGCATGCGTTTCGGGAAGTAAAACCTCAAGTTCGCTGAAGCCGT  2665
            |||||
Db    1740  ATTTCAGCGTCCTGCCTGGACGGCTATCACGCGTAAATGCGTTGGGTGCAGACTACAGCTGT  1799

Qy    2666  GAGCCAAGTGGCGGCGCACACGGTGCCACTGTGTGGGGTCAGACTATCAGCTGTTGCTGGT  2725
            ||||||||||||||||
Db    1800  ACTGCCGCTGTTGCAAGACGATGACATTATCGGATCCACGATTATCACCTGTTGCCATT  1859

Qy    2726  TCCTGGCATTTGCGGCCAGATGCGCCCTGATTGAAGATCGGTTTCTTCCTCCACATTCC  2785
            |||||||||||
Db    1860  TGCGCATGAATTACGCAAACGGGAGTGAATAATCGCATTGGTTTCTTTCTGCATATTCC  1919

Qy    2786  CTTCCCTTCCCGATCTGTTCCGTCAGCTGC  2817
            |||||||
Db    1920  TTTCCCGACACCGGAAATCTTCAACGCGCTGC  1951
```

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RESULT 10
US-09-489-039A-7037
; Sequence 7037, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
;    APPLICANT: Gary Breton et. al
;    TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
;    TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
;    FILE REFERENCE: 2709.2004001
;    CURRENT APPLICATION NUMBER: US/09/489,039A
;    CURRENT FILING DATE: 2000-01-27
;    PRIOR APPLICATION NUMBER: US 60/117,747
;    PRIOR FILING DATE: 1999-01-29
;    NUMBER OF SEQ ID NOS: 14342
;    SEQ ID NO 7037
;    LENGTH: 1479
;    TYPE: DNA
;    ORGANISM: Klebsiella pneumoniae
US-09-489-039A-7037

Query Match         2.5%;    Score 70.2;    DB 4;    Length 1479;
Best Local Similarity   52.6%;    Pred. No. 4.2e-12;
Matches 153;    Conservative 0;    Mismatches 138;    Indels 0;    Gaps 0;

Qy    2516  CCTCACTGCAAGTGACTATGAAGGCTTCTACGAGGGCTTTCAAACGCAACGGCGTGTGGCC  2575
            ||||||||||||||||||||||||||||
Db    255   CCTTAATGAACGGGACCATGATGAATACTACAACCAGTTCTTAACGCGTGCTGTGCGCC  314

Qy    2576  TCTTTTCCACGATTTGATTGTTACTCCGGTGTACAAACACCGATTGGTGTGCAAGCATGCGTTTCG  2635
            ||||||||                    |||      ||||
Db    315   GGCTTTCCACTATCGCCTTGATCTGGTCGGTCAGCTTGCCGGCGGAAGCCTGGGAGGGATATCT  374
```

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Qy    2492  GGGTG------TTTTGCTGCGCACCCTGTTGTCCTCACTGCAAGTGACTATGAAGGGCTTCTA  2545
            ||||                   ||||||||||||
Db    195   AAAAGGTAACATTACGTCGGCCTCTTTTAACCTCAGCGAACAGGACCTTGACGAATACTA  254

Qy    2546  CGAGGGCTTTCAAACGCAACGGTGTGGCCCTCTTTTTCCACGATTTGATTGTTACTCCGGT  2605
            ||||||||||||||||||||||||||||||||||
Db    255   CAACCAATTCTCCAATGCCGTTCTCTGGCCCGCGTTTCATTATCGGCTCGATCGGTGTGCA  314

Qy    2606  GTACACACCGATTGGTGGCATGCGTTTCGGGAAGTAAACCTCAAGTTCGCTGAAGCCGT  2665
            ||||||
Db    315   ATTTCAGCGTCCTGCCTGGGACGGCGTTATCACGCGTAAATGCGTAAATGCGTGTTGCTGGT  374

Qy    2666  GAGCCAAGTGGGCGGCACACGGTGCCACTGTGTGGGGTCAGACTATCAGCTGTTGCTGGT  2725
            |||||
Db    375   ACTGCCGCTGTTGCAAGACGATGACATTATCTGGATCCACGATTATCACCTGTTGCCATT  434

Qy    2726  TCCTGGCATTTGCGGCCACTGTGTGGGGCCAGACTATCAGCTGTTGCTGGT  2785
            |||||         ||||||||||||||||||||
Db    435   TGCGCATGAATTACGCAAACGGGAGTGAATAATCGCATTGGTTTCTTTCTGCATATTCC  494

Qy    2786  CTTCCCTTCCCGATCTGTTCCGTCAGCTGC  2817
            |||||||
Db    495   TTTCCCGACACCGGAAATCTTCAACGCGCTGC  526
```

```
RESULT 9
US-08-274-121B-1
; Sequence 1, Application US/08274121B
; Patent No. 6133034
; GENERAL INFORMATION:
;    APPLICANT: Arne Reidar Strom
;    APPLICANT: Inga Kaasen
;    APPLICANT: Olaf Bay Styrvold
;    APPLICANT: John McDougall
;    TITLE OF INVENTION: Methods and Compositions
;    TITLE OF INVENTION: Related To The Production
;    TITLE OF INVENTION: of Trehalose
;    NUMBER OF SEQUENCES: 6
;    CORRESPONDENCE ADDRESS:
;       ADDRESSEE: Calgene, Inc.
;       STREET: 1920 Fifth Street
;       CITY: Davis
;       STATE: CA
;       COUNTRY: USA
;       ZIP: 95616
;    COMPUTER READABLE FORM:
;       MEDIUM TYPE: Diskette, 3.50 inch, 2.0 MB
;       COMPUTER: Apple Macintosh
;       OPERATING SYSTEM: Macintosh 7.1
;       SOFTWARE: Microsoft Word 5.1(a)
;    CURRENT APPLICATION DATA:
;       APPLICATION NUMBER: US/08/274,121B
;       FILING DATE: 12-JULY-1994
;       CLASSIFICATION: 435
;    PRIOR APPLICATION DATA:
;       APPLICATION NUMBER: 07/893,099
;       FILING DATE: 27-MAY-1992
;       CLASSIFICATION: 435
;    ATTORNEY/AGENT INFORMATION:
;       NAME: Elizabeth Lassen
;       REGISTRATION NUMBER: 31,845
;       NAME: Donna E. Scherer
;       REGISTRATION NUMBER: 34,719
;       REFERENCE/DOCKET NUMBER: CGNE 86(1)
;    TELECOMMUNICATION INFORMATION:
;       TELEPHONE: (916) 753-6313
;       TELEFAX: (916) 753-1510
; INFORMATION FOR SEQ ID NO: 1:
;    SEQUENCE CHARACTERISTICS:
;       LENGTH: 2868 base pairs
;       TYPE: nucleic acid
;       STRANDEDNESS: double
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Qy   2636  GGAAGTAAACCTCAAGTTCGCTGAAGCCGTGAGCCAAGTGCGGCACACGGTGCCACTGT  2695
            ||||| ||||||||||||||||| |||| || |||||||||| || |||||||||||||
Db    375  GCGGGTTAACGCCATGCATCAGCTTGTGTTCCTGGCATTTGCGCCAGACGATACGCT   434

Qy   2696  GTGGGGTGCAGGACTATCAGCTTGTGTTCGTGGTTCCTGGCATTTGCGCCAGATGCGCCCTGA  2755
            |||||||||||||||||||||||||||||||||
Db    435  GTGGATCCATGATTACCATCTTCTGCCCTTCGCCAGCGAGCTGCGCAAGCGCGGGGTGAA   494

Qy   2756  TTTGAAGATCGGTTTCTTCCTCCACAATTCCCTTCCCTTCCCGACGCGCCGAGATTTT  2806
            ||||||||||||||||||||||||||||||||||||
Db    495  CAATCGGATCCGGTTTTTTCTTACATATTCCGTTCCCGACGCGCCGAGATTTT   545
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RESULT 11
US-09-328-352-595
; Sequence 595, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
;   APPLICANT: Gary L. Breton et al.
;   TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
;   TITLE OF INVENTION: BAUMANNI FOR DIAGNOSTICS AND THERAPEUTICS
;   FILE REFERENCE: GTC99-03PA
;   CURRENT APPLICATION NUMBER: US/09/328,352
;   CURRENT FILING DATE: 1999-06-04
;   NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 595
;   LENGTH: 1455
;   TYPE: DNA
;   ORGANISM: Acinetobacter baumannii
US-09-328-352-595

Query Match   2.0%;   Score 56; DB 4; Length 1455;
Best Local Similarity   49.7%;   Pred. No. 2.1e-07;
Matches   143;   Conservative   0;   Mismatches   145;   Indels   0;   Gaps   0;

```
Qy   2530  ACTATGAAGGCTTCTACGAGGGCTTTTCAAACGCAACGCTGTGGCCTCTTTTCCACGATT  2589
            ||||| || ||||||   | |||||
Db    242  AATATGCACAGTACTACTGTGTTTTGCCAATAAAGTATTATGGCCTGCCATGCATGATC   301

Qy   2590  TGATTGTTACTCCGGTGTACACACCGATTGGTGGCATGCGTTTCGGGAAGTAAACCTCA  2649
            ||| |||||
Db    302  GGGATGACCTGATCGATCGAATATATATAACGCAGAAGAATATATAACCTACCAAAAGGTCAATCTGTT   361

Qy   2650  AGTTCGCTGAAGCCGTGAGCCAAGTGCGGCACACGGTGCCACTGTGTGGGGTGCAGGACT  2709
            |||||
Db    362  TATTTGCTGAAAAATTACAACAGATTGCTCAGCCTGATGATCTGATTTGGGTGCATGACT   421

Qy   2710  ATCAGCTGTTGCTGGTTCCTGGCATTTGCGCCAGATGCGCCCTGATTTGAAGATCGGTT  2769
            |||||      ||| |||||||
Db    422  ATCACTTTTCAGCGTAGCTCGTCCGTCATTGCCGTGAATTAGGTATGCAAAATAAAATCGGTT   481

Qy   2770  TCTTCCTCCACAATTCCCTTCCCTTCCCTTCCCGATCGTGTCGTCAGCTGC  2817
            ||| || ||||||||
Db    482  TCTTTTGCATATTCCTTTCCTTTCGCAAGCTTAAATATCTGGCGCAAGATCC   529
```

RESULT 12
US-09-248-796A-3169
; Sequence 3169, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
;   APPLICANT: Keith Weinstock et al
;   TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
;   TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
;   FILE REFERENCE: 107196.132
;   CURRENT APPLICATION NUMBER: US/09/248,796A
;   CURRENT FILING DATE: 1999-02-12
;   PRIOR APPLICATION NUMBER: US 60/074,725
;   PRIOR APPLICATION FILING DATE: 1998-02-13
;   PRIOR APPLICATION NUMBER: US 60/096,409
;   PRIOR APPLICATION FILING DATE: 1998-08-13
;   NUMBER OF SEQ ID NOS: 3169
; SEQ ID NO 3169

;   LENGTH: 2241
;   TYPE: DNA
;   ORGANISM: Candida albicans
US-09-248-796A-3169

Query Match   1.9%;   Score 54.8; DB 4; Length 2241;
Best Local Similarity   58.6%;   Pred. No. 7.6e-07;
Matches   95;   Conservative   0;   Mismatches   67;   Indels   0;   Gaps   0;

```
Qy   2649  AAGTTCGCTGAAGCCGTGAGCCAAGTGGCGGCACACGGTGCCACTGTGTGGGGTGCAGGAC  2708
            ||||| ||||    |  |||||  ||  ||||  |
Db    268  AAAATAGTGGAAACATACAACGACGTGAATGATGATGAAGAGACAACTGTATGGATTCATGAC   327

Qy   2709  TATCAGCTGTTGCTGGTTCCTGGCATTTGCGCCAGATGCGCCCTGATTTGAAGATCGGT  2768
            ||||| ||  |   ||||||
Db    328  TACCACTTGTTATTAGTTCCCAAGATGGTTCGCGACAAGTTGCCTAATCGAAAAATCGGG   387

Qy   2769  TTCTTCCCCACATTCCCTTCCCTTCCCTGATCGTGTTCCGT  2810
            |||||||||||   |||||||||||||||||||||||||||
Db    388  TTTTTCTTGCATGTGTCTTTCCCCTTTCTTCAGAAGTTTTCCGT   429
```

RESULT 13
US-09-614-221A-160
; Sequence 160, Application US/09614221A
; Patent No. 6723837
; GENERAL INFORMATION:
;   APPLICANT: Karunanandaa, Balasulojini
;   APPLICANT: Yu, Jaehyuk
;   APPLICANT: Kishore, Ganesh M.
;   TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED
;   TITLE OF INVENTION: WITH STEROL SYNTHESIS AND METABOLISM
;   FILE REFERENCE: 16516.075
;   CURRENT APPLICATION NUMBER: US/09/614,221A
;   CURRENT FILING DATE: 2000-07-12
;   PRIOR APPLICATION NUMBER: US 60/142,981
;   PRIOR FILING DATE: 1999-07-12
;   NUMBER OF SEQ ID NOS: 626
; SEQ ID NO 160
;   LENGTH: 3165
;   TYPE: DNA
;   ORGANISM: Saccharomyces cerevisiae
US-09-614-221A-160

Query Match   1.9%;   Score 52.6; DB 4; Length 3165;
Best Local Similarity   49.1%;   Pred. No. 5.4e-06;
Matches   139;   Conservative   0;   Mismatches   144;   Indels   0;   Gaps   0;

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Qy   2527  GTGACTATGAAGGCTTCTACGAGGGCTTTTCAAACGCAACGCTGTGGCCTCTTTTCCACG  2586
            ||||||       ||||
Db   1157  GTGCTTATAAGAACTACGCCAAACAGATTTTATGGCCCATTCATTATCAAATTCCAG  1216

Qy   2587  ATTTGATTGTTACTCCGGTGTACAACACCGATTGGTGGCATGCGTTTCGGGAAGTAAACC  2646
            ||| |||||||
Db   1217  ATAATCCAAATTCAAAGGCTTTTGAAGACCATTCTTGGGACTACTACTATCAAAAAGTGAATC  1276

Qy   2647  TCAAGTTCGCTGAAGCCGTGAGCCAAGTGGCGGCACACGGTGCCACTGTGTGGGGTGCAGG  2706
            ||||| ||
Db   1277  AAAAGTTTTCTGATAGGATAGTTTCCGTTACAAACCTGGCGACACAATTTGATCCATG  1336

Qy   2707  ACTATCAGCTGTTGCTGGTTCCTGGCATTTGCGCCAGATGCGCCCTGATTTGAAGATCG  2766
            |||||
Db   1337  ATTATCATTTGATGCTTGTCCCACAAATGGTGAGAGAAACTGCCTAAAGCTAAGATTG  1396

Qy   2767  GTTTCTTCCTCCACATTCCCTTCCCTTCCCTGATCTGTTCCG  2809
            |||
Db   1397  GATTTTTCTTACACGTATCATTTCCAAGTAGTAGGTCTTCAG  1439
```

RESULT 14
US-09-651-169A-36
; Sequence 36, Application US/09651169A
; Patent No. 6505565

```
;   GENERAL INFORMATION:
;   APPLICANT: Conner, Timothy W
;   APPLICANT: Tzafrir, Iris
;   TITLE OF INVENTION: Plant Regulatory Sequences for Selective Control of Gene Expressi
;   FILE REFERENCE: 06009.0019.NPUS00 (RENN:019)
;   CURRENT APPLICATION NUMBER: US/09/651,169A
;   CURRENT FILING DATE: 2000-08-30
;   NUMBER OF SEQ ID NOS: 51
;   SOFTWARE: PatentIn version 3.0
;   SEQ ID NO 36
;   LENGTH: 654
;   TYPE: DNA
;   ORGANISM: Zea Mays
US-09-651-169A-36

Query Match          1.7%;   Score 48; DB 4; Length 654;
Best Local Similarity  51.4%;   Pred. No. 5.1e-05;
Matches 108; Conservative  1; Mismatches 101;  Indels  0;  Gaps  0;

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Qy  2728 CTGGCATTTTGCGCCAGATGCGCCCTGATTTGAAGATCGGTTTCTTCCTCCACATTCCCT 2787
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RESULT 15
US-08-232-463-14
; Sequence 14, Application US/08232463
; Patent No. 5670367
;   GENERAL INFORMATION:
;   APPLICANT: DORNER, F.
;   APPLICANT: SCHEIFLINGER, F.
;   APPLICANT: FALKNER, F. G.
;   TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
;   NUMBER OF SEQUENCES: 52
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Foley & Lardner
;   STREET: 1800 Diagonal Road, Suite 500
;   CITY: Alexandria
;   STATE: VA
;   COUNTRY: USA
;   ZIP: 22313-0299
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/232,463
;   FILING DATE:
;   CLASSIFICATION: 435
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US/07/935,313
;   FILING DATE:
;   APPLICATION NUMBER: EP 91 114 300.6
;   FILING DATE: 26-AUG-1991
;   ATTORNEY/AGENT INFORMATION:
;   NAME: BENT, Stephen A.
;   REGISTRATION NUMBER: 29,768
;   REFERENCE/DOCKET NUMBER: 30472/114 IMMU
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (703)836-9300
```

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;   TELEFAX: (703)683-4109
;   TELEX: 899149
; INFORMATION FOR SEQ ID NO: 14:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 7218 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   IMMEDIATE SOURCE:
;   CLONE: pTZgpt-F18
US-08-232-463-14

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Search completed: January 14, 2005, 10:08:45
Job time : 262.002 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: January 14, 2005, 09:56:14 ; Search time 1431.15 Seconds
(without alignments)
11309.899 Million cell updates/sec

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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4300275 seqs, 2872944193 residues

Total number of hits satisfying chosen parameters: 8600550

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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3	2817	100.0	2817	9	US-09-834-721-1	Sequence 1, Appli
4	2817	100.0	2817	9	US-09-783-388-1	Sequence 1, Appli
5	2817	100.0	2817	10	US-09-951-535-1	Sequence 9, Appli
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7	2783.4	98.8	3309400	9	US-09-738-626-1	Sequence 1, Appli
8	1836.6	65.2	1909	9	US-09-951-536-3	Sequence 3, Appli
9	1836.6	65.2	1909	9	US-09-963-521-3	Sequence 3, Appli
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12	1836.6	65.2	1909	10	US-09-951-535-3	Sequence 3, Appli
13		1836.6	65.2	1909	17	US-10-224-574-11	Sequence 11, Appl
14		1561.2	55.4	1590	16	US-10-627-476-557	Sequence 557, App
15		1561.2	55.4	1590	16	US-10-450-055-41	Sequence 41, Appl
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35		74.2	2.6	1356	15	US-10-369-493-39284	Sequence 39284, A
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43		68.2	2.4	1374	15	US-10-369-493-28062	Sequence 28062, A
44		68.2	2.4	1374	15	US-10-369-493-30816	Sequence 30816, A
45		66.2	2.4	1389	15	US-10-156-761-3920	Sequence 3920, Ap

ALIGNMENTS

RESULT 1
US-09-951-536-1
; Sequence 1, Application US/09951536
; Patent No. US2002010737S8A1
; GENERAL INFORMATION:
; APPLICANT: ZIEGLER, PETRA
; APPLICANT: EGGELING, LOTHAR
; APPLICANT: SAHM, HERMANN
; APPLICANT: THIERBACH, GEORG
; TITLE OF INVENTION: NEW NUCLEOTIDE SEQUENCES CODING FOR THE THRE GENE AND
; TITLE OF INVENTION: PROCESS FOR THE ENZYMATIC PRODUCTION OF L-THREONINE
; TITLE OF INVENTION: USING CORYNEFORM BACTERIA
; FILE REFERENCE: 21123/282414/MAS
; CURRENT APPLICATION NUMBER: US/09/951,536
; CURRENT FILING DATE: 2001-09-14
; PRIOR APPLICATION NUMBER: 09/431,099
; PRIOR FILING DATE: 1999-11-01
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
US-09-951-536-1
SEQ ID NO 1
; LENGTH: 2817
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (398)..(1864)
; OTHER INFORMATION: thrE-Gen
US-09-951-536-1

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Best Local Similarity 100.0%; Pred. No. 0;
Matches 2817; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy  841 GTCTTATGGTTTCCCGTGCGTTGGCGCGGCAATGATGAGGGTGGCGCGTGTTGCTGT 900
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  841 GTCTTATGGTTTCCCGTGCGTTGGCGCGGCAATGATGAGGGTGGCGCGTGTTGCTGT 900

Qy  901 GCTGTTTGGCGTCATTTTTGGGAATGGCAGGTTTCCCTAATTGCTTTATTACCGCGTTCACGATCAT 960
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  901 GCTGTTTGGGATGGCAGGTTTCCCTAATTGCTTTATTACCGCGTTCACGATCAT 960

Qy  961 TGCCACGACGTCATTTTTGGGAAAGAGAGGGTTTGCCTACTCTTCTTCGGCGTTGCAAAATGTTGTTGG 1020
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  961 TGCCACGACGTCATTTTTGGGAAAGAGAGGGTTTGCCTACTCTTCTTCGGCGTTGCAAAATGTTGTTGG 1020

Qy 1021 TGGTTTTATTGCCACGCTGCCTGCCATCGATTGCTTATTCTTTGGCGTTGCAATTTGGTCT 1080
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1021 TGGTTTTATTGCCACGCTGCCCTGCCATCGATTGCTTATTCTTTGGCGTTGCAATTTGGTCT 1080

Qy 1081 TGAGATCAAACCGAGCCAGATCATCATCGGGAATTGGTGTGTCGTGTTGGCAGGTTTGAC 1140
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1081 TGAGATCAAACCGAGCCAGATCATCATCGGGAATTGGTGTGTCGTGTTGGCAGGTTTGAC 1140
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Matches 2817;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

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Qy     1 AATGAAATAATCCCCTCACCAACTGGCGACATTCAAACACCGTTTCATTTCCAAACATCG   60
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Db     1 AATGAAATAATCCCCTCACCAACTGGCGACATTCAAACACCGTTTCATTTCCAAACATCG   60

Qy    61 AGCCAAGGGAAAAGAAAGCCCCTTAAGCCCGTGTTATTAAATGGAGACTCTTTGGAGACC  120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61 AGCCAAGGGAAAAGAAAGCCCCTTAAGCCCGTGTTATTAAATGGAGACTCTTTGGAGACC  120

Qy   121 TCAAGCCAAAAGGGGCATTTCATTAAGAAAATACCCCTTGACCTGGTGTTATTGAGC     180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 TCAAGCCAAAAGGGGCATTTCATTAAGAAAATACCCCTTGACCTGGTGTTATTGAGC     180

Qy   181 TGGAAGAGAGACTTGAACCTGCAATTAACAACTACGAATCACAGTGCGTTGCGTGCCAATTGCG  240
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 TGGAAGAGAGACTTGAACCTGCAATTAACAACTACGAATCACAGTGCGTTGCGTGCCAATTGCG  240

Qy   241 CCACTCCAGCACCGCAGATGCTGATGATCAACAACTACGAATACGTATCTTAGCGTATGT  300
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 CCACTCCAGCACCGCAGATGCTGATGATCAACAACTACGAATACGTATCTTAGCGTATGT  300

Qy   301 GTACATCACAATGGAATTCGGGGCTAGAGTATCTGGTGAACCGTGCATAAACGACCTGTG  360
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 GTACATCACAATGGAATTCGGGGCTAGAGTATCTGGTGAACCGTGCATAAACGACCTGTG  360

Qy   361 ATTGGACTCTTTTCCTTGCAAAATGTTTTCCAGCGATGTTGGCGACCCTTCG         420
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 ATTGGACTCTTTTCCTTGCAAAATGTTTTCCAGCGATGTTGGCGACCCTTCG         420

Qy   421 TGGCCGCATTTCAACAGTTGACGCTGCAAAAGCCGCACCTCCGCCATCGCCACTAGCCCC  480
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 TGGCCGCATTTCAACAGTTGACGCTGCAAAAGCCGCACCTCCGCCATCGCCACTAGCCCC  480

Qy   481 GATTGATCTCACTGACCATAGTCAAGTGCCGGTGTGATGAATTGGCTGCGAGAATTGG    540
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 GATTGATCTCACTGACCATAGTCAAGTGCCGGTGTGATGAATTGGCTGCGAGAATTGG    540

Qy   541 CGATATTTTGCTTTCTTCAGGTACGTCAAACAGTGATCAAACAGTGATACCAAGGTGCGAGCGGT  600
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541 CGATATTTTGCTTTCTTCAGGTACGTCAAACAGTGATCAAACAGTGATACCAAGGTGCGAGCGGT  600

Qy   601 GACCTCTGCGTATGGCCTGTACTATACGCATGTGGATATCACGTTGAATACGATCACCAT  660
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601 GACCTCTGCGTATGGCCTGTACTATACGCATGTGGATATCACGTTGAATACGATCACCAT  660

Qy   661 CTTCACCAACATCGGTGTGGAGGAAGATGGCCGGTCAACGTGTTCATGTTGTGGGCAA    720
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   661 CTTCACCAACATCGGTGTGGAGGAAGATGGCCGGTCAACGTGTTCATGTTGTGGGCAA    720

Qy   721 GTTGGACACCAACTTCTCCCAAACTGTCTGGAGGTTGACCGTTTGAGTCCATTCAGGC   780
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   721 GTTGGACACCAACTTCTCCCAAACTGTCTGGAGGTTGACCGTTTGAGTCCATTCAGGC   780

Qy   781 TGGTGCTACCCCGCCTGAGGTTGCCGACGAGTTGGAGCAATCGCCTGC            840
         ||||||||||||||||||||||||||||||||||||||||||||||||
Db   781 TGGTGCTACCCCGCCTGAGGTTGCCGACGAGTTGGAGCAATCGCCTGC            840

Qy   841 GTCTTATGGTTTCCCGTTGCGTTGCCTGGCCAATGATGGGTGGGCCTGTTGCTGT      900
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   841 GTCTTATGGTTTCCCGTTGCGTTGCCTGGCCAATGATGGGTGGGCCTGTTGCTGT      900

Qy   901 GCTGTTGGGTGGTGGATGGCAGGTTTCCCTAATTGCTTTTATTACCGCGTTCACGGATCAT  960
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   901 GCTGTTGGGTGGTGGATGGCAGGTTTCCCTAATTGCTTTTATTACCGCGTTCACGGATCAT  960

Qy   961 TGCCACGACGTCATTTTGGGAAAGAGAGGGTTTGCCTACTTTCTTCCAAAATGTTGTTGG 1020
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   961 TGCCACGACGTCATTTTGGGAAAGAGAGGGTTTGCCTACTTTCTTCCAAAATGTTGTTGG 1020

Qy  1021 TGGTTTTATTGCCACGCTGCCTCGCATCGATTGCTTATTCTTTGGCGTTGCAATTTGGTCT 1080
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1021 TGGTTTTATTGCCACGCTGCCTCGCATCGATTGCTTATTCTTTGGCGTTGCAATTTGGTCT 1080
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Qy  2221 CCACTAAGAAACTACTAAAAAGACCACCGCAAAGAAGAAGCCACAAAGAAGTCTTAAGCCG 2280
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2221 CCACTAAGAAACTACTAAAAAGACCACCGCAAAGAAGAAGCCACAAAGAAGTCTTAAGCCG 2280

Qy  2281 GATCTTATATGATGATTCCAATAGCTTTGTAGTTGTTGCTAACCGTCTGCCAGTGGATA   2340
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2281 GATCTTATATGATGATTCCAATAGCTTTGTAGTTGTTGCTAACCGTCTGCCAGTGGATA   2340

Qy  2341 TGACTGTCCACCCAGATGGTAGCTATAGCATCTCCCCAGCCCGGCCTTGTCACGG      2400
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2341 TGACTGTCCACCCAGATGGTAGCTATAGCATCTCCCCAGCCCGGCCTTGTCACGG      2400

Qy  2401 GGCTTTCCCCCGGTTCTGGAACAACATCGTGGATGTTGGGTCGGATGGCCTGGAACTGTAG 2460
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2401 GGCTTTCCCCCGGTTCTGGAACAACATCGTGGATGTTGGGTCGGATGGCCTGGAACTGTAG 2460

Qy  2461 ATGTTGCACCGGAACCATTTCGAACAGATACGGGTGTTTTGCTCGCACCCTGTTGTCCTCA 2520
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2461 ATGTTGCACCGGAACCATTTCGAACAGATACGGGTGTTTTGCTCGCACCCTGTTGTCCTCA 2520

Qy  2521 CTGCAAGTGACTATGAAGGCTTCTACGAGGGCTTTTCAAACGCAACGCTGTTGGCCTCTTT 2580
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2521 CTGCAAGTGACTATGAAGGCTTCTACGAGGGCTTTTCAAACGCAACGCTGTTGGCCTCTTT 2580

Qy  2581 TCCACGATTTGATTGTTACTCCGGTGTACACACCGATTGGTGGCATGCGTTTCGGGAAG   2640
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2581 TCCACGATTTGATTGTTACTCCGGTGTACACACCGATTGGTGGCATGCGTTTCGGGAAG   2640

Qy  2641 TAAACCTCAAGTTCGCTGAAGCCGTGAGCCAAGTGGCGCACACGGTGCCACTGTGTGGG   2700
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2641 TAAACCTCAAGTTCGCTGAAGCCGTGAGCCAAGTGGCGCACACGGTGCCACTGTGTGGG   2700

Qy  2701 TGCAGGACTATCAGCTGTTGTGCTGGTTCCTGGCATTTGCGCCGCAGATGCGCCCTGATTTGA 2760
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2701 TGCAGGACTATCAGCTGTTGTGCTGGTTCCTGGCATTTGCGCCGCAGATGCGCCCTGATTTGA 2760

Qy  2761 AGATCGGTTTCTTCCTTCCCCACATTCCCTTCCCCTTCCCCTGATCGTGTTCCGTCAGCTGC 2817
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2761 AGATCGGTTTCTTCCTTCCCCACATTCCCTTCCCCTTCCCCTGATCGTGTTCCGTCAGCTGC 2817
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RESULT 2
US-09-963-521-1
; Sequence 1, Application US/09963521
; Patent No. US2002014678lAl
; GENERAL INFORMATION:
; APPLICANT: ZIEGLER, PETRA
; APPLICANT: EGGELING, LOTHAR
; APPLICANT: SAHM, HERMANN
; TITLE OF INVENTION: NEW NUCLEOTIDE SEQUENCES CODING FOR THE THRE GENE
; TITLE OF INVENTION: AND PROCESS FOR THE ENZYMATIC PRODUCTION OF
; TITLE OF INVENTION: L-THREONINE USING CORYNEFORM BACTERIA
; FILE REFERENCE: 21123/282413/MAS
; CURRENT APPLICATION NUMBER: US/09/963,521
; CURRENT FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: 09/431,099
; PRIOR FILING DATE: 1999-11-01
; PRIOR APPLICATION NUMBER: DE 199 41 478.5
; PRIOR FILING DATE: 1999-09-01
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 2817
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (398)..(1864)
; OTHER INFORMATION: thrE-Gen
US-09-963-521-1

Query Match   100.0%;   Score 2817;   DB 9;   Length 2817;
Best Local Similarity 100.0%;   Pred. No. 0;

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Qy   1081  TGAGATCAAACCGAGCCAGATCATCGCATCTGGAATTGTTGTGCGTGTTGGCAGGTTTGAC  1140
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081  TGAGATCAAACCGAGCCAGATCATCGCATCTGGAATTGTTGTGCGTGTTGGCAGGTTTGAC  1140

Qy   1141  ACTTGTGCAATCTCTGCGAGGACGGCATCACGCGGCGCCTCCGGTGACAGCAAGTCGACGATT  1200
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141  ACTTGTGCAATCTCTGCGAGGACGGCATCACGCGGCGCCTCCGGTGACAGCAAGTCGACGATT  1200

Qy   1201  TTTTGAAACACTCCGTGTTTACCGGCGTGGCATTGTTGCTGGCGTGGGTTTGGGCATTCAGCT  1260
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1201  TTTTGAAACACTCCGTGTTTACCGGCGTGGCATTGTTGCTGGCGTGGGTTTGGGCATTCAGCT  1260

Qy   1261  TTCTGAAATCTTGCATGTCATGTTGCCTGCCATGGAGTTCCGCTGCAGCACCTTAATTATTC  1320
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1261  TTCTGAAATCTTGCATGTCATGTTGCCTGCCATGGAGTTCCGCTGCAGCACCTTAATTATTC  1320

Qy   1321  GTCTACATTCGCCCGCCATTATCGCTGGTGGCGTCACCGCAGCCGCCTTCGCAGTGGGGTTG  1380
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1321  GTCTACATTCGCCCGCCATTATCGCTGGTGGCGTCACCGCAGCCGCCTTCGCAGTGGGGTTG  1380

Qy   1381  TTACGCGGAGTGGTCCTCGGTGATTATTGCGGGCCTTACTGCCGCTGATGGGTTCTGCGTT  1440
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1381  TTACGCGGAGTGGTCCTCGGTGATTATTGCGGGCCTTACTGCCGCTGATGGGTTCTGCGTT  1440

Qy   1441  TTATTACCTTCTTCGTTGTTTATTTAGGCCCCGTCTCTGCCGATTGCTGCAACAGC  1500
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1441  TTATTACCTTCTTCGTTGTTTATTTAGGCCCCGTCTCTGCCGATTGCTGCAACAGC  1500

Qy   1501  AGTTGGTTCACTGGTGGTTTGCTTGCCCGTCGATTCTTGATTCCACCGTTGATTGTGGC  1560
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1501  AGTTGGTTCACTGGTGGTTTGCTTGCCCGTCGATTCTTGATTCCACCGTTGATTGTGGC  1560

Qy   1561  GATTGCCCGGCATCACACCAAATGCTTCCAGGTCTAGCAATTTACCGCGGAATGTACGGCCAC  1620
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1561  GATTGCCCGGCATCACACCAAATGCTTCCAGGTCTAGCAATTTACCGCGGAATGTACGGCCAC  1620

Qy   1621  CTTGAATGATCAAAACACTCATGGTTTCACCCAACATTGCGGTTGCTTTAGCCACTGCTTC  1680
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1621  CTTGAATGATCAAAACACTCATGGTTTCACCCAACATTGCGGTTGCTTTAGCCACTGCTTC  1680

Qy   1681  ATCACTTGCCGCGCTGGCGCTGGTTTGGGTGAGTGGATTGCCCCGCAGGCTACGTCGTCCACC  1740
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1681  ATCACTTGCCGCGCTGGCGCTGGTTTGGGTGAGTGGATTGCCCCGCAGGCTACGTCGTCCACC  1740

Qy   1741  ACGCTTCAACCCATACCGTGCATTTACCAAGGCGAATGAGTTCTCCTTCCAGGAGGAAGC  1800
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1741  ACGCTTCAACCCATACCGTGCATTTACCAAGGCGAATGAGTTCTCCTTCCAGGAGGAAGC  1800

Qy   1801  TGAGCAGAATCAGCGCGCCGGCGAGAGAAAACGTCCAAAGACTAATCAAAGATTCGGTAATAA  1860
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1801  TGAGCAGAATCAGCGCGCCGGCGAGAGAAAACGTCCAAAGACTAATCAAAGATTCGGTAATAA  1860

Qy   1861  AAGGTAAAAATCAACCTGCTTAGGCGTCTTTCGCTTAAATAGCGTAGAAATATCGGGTCGA  1920
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1861  AAGGTAAAAATCAACCTGCTTAGGCGTCTTTCGCTTAAATAGCGTAGAAATATCGGGTCGA  1920

Qy   1921  TCGCTTTAAACACTCAGGAGGATCCTTGCCGCGCCAAAATCACGGACACTCGTCCACCC  1980
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1921  TCGCTTTAAACACTCAGGAGGATCCTTGCCGCGCCAAAATCACGGACACTCGTCCACCC  1980

Qy   1981  CAGAATCCCTTCACGCGTGTTGAAGAGAGAAACCGCAGCCGGCGGGATTGTTGCCA  2040
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1981  CAGAATCCCTTCACGCGTGTTGAAGAGAGAAACCGCAGCCGGCGGGATTGTTGCCA  2040

Qy   2041  CCTATTCTCAAGGACTTCTTCGACGGCGTCACTTTGATTGCATGCGGCGGTTGAACCTC  2100
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2041  CCTATTCTCAAGGACTTCTTCGACGGCGTCACTTTGATTGCATGCGGCGGTTGAACCTC  2100

Qy   2101  AGGGCCTGCGTTACACCCAAGGTCGCTTCTGAACACGAGGAAGCTCAGCCAAAGAGGCTA  2160
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2101  AGGGCCTGCGTTACACCCAAGGTCGCTTCTGAACACGAGGAAGCTCAGCCAAAGAGGCTA  2160
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Qy   2161  CAAAGGCGGACTCGTCGTAAGGCACCAGCTAAGAAGGCTGCTCGCTAAGAAACACCAAGAAGA  2220
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2161  CAAAGGCGGACTCGTCGTAAGGCACCAGCTAAGAAGGCTGCTCGCTAAGAAACACCAAGAAGA  2220

Qy   2221  CCACTAAGAAAACTACTAAAAGAACCACCGCAAAGAACCACCGCAAAGAGAGTCTTAAGCCG  2280
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2221  CCACTAAGAAAACTACTAAAAGAACCACCGCAAAGAACCACCGCAAAGAGAGTCTTAAGCCG  2280

Qy   2281  GATCTTATATGGATGATTCCAATAGCTTTGTAGTTGTTGCTAACCGTCTCGCCAGTGGATA  2340
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2281  GATCTTATATGGATGATTCCAATAGCTTTGTAGTTGTTGCTAACCGTCTCGCCAGTGGATA  2340

Qy   2341  TGACTGTCCACCCAGATGTGAGTAGTAGACATCGTGGGCGTAGACAACATCGTGGATGTTGG  2400
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2341  TGACTGTCCACCCAGATGTGAGTAGTAGACATCGTGGGCGTAGACAACATCGTGGATGTTGG  2400

Qy   2401  GGCTTTCCCCGTTCTGGAACAACATCGTGGATGTTGGGTCGGATGGCCTTGGCTCGGATAGGCCTCGGGAAG  2460
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2401  GGCTTTCCCCGTTCTGGAACAACATCGTGGATGTTGGGTCGGATGGCCTTGGCTCGGATAGGCCTCGGGAAG  2460

Qy   2461  ATGTTGCACCCGAACCATTTCGAACAGATACGGGTGTTTTGCTGCCCTGTTGTGTCCTCA  2520
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2461  ATGTTGCACCCGAACCATTTCGAACAGATACGGGTGTTTTGCTGCCCTGTTGTGTCCTCA  2520

Qy   2521  CTGCAAGTGACTATGAAGGCTTCTACGAGGGGCTTTCAAACGCAACGCGTGTGGCCTCTTT  2580
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2521  CTGCAAGTGACTATGAAGGCTTCTACGAGGGGCTTTCAAACGCAACGCGTGTGGCCTCTTT  2580

Qy   2581  TCCACGATTGATTGTTACTCCGGTGTACAACACCGATTGGTGGCATGCGTTTCGGGAAG  2640
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2581  TCCACGATTGATTGTTACTCCGGTGTACAACACCGATTGGTGGCATGCGTTTCGGGAG  2640

Qy   2641  TAAACCTTCAAGTTCGCTGAAGCCGTGAGCGAGCCAAGTGGCACGGTGCCACTGTGTGGG  2700
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2641  TAAACCTTCAAGTTCGCTGAAGCCGTGAGCGAGCCAAGTGGCACGGTGCCACTGTGTGGG  2700

Qy   2701  TGCAGGACTATCAGCGTGTTGCTGGTTCCTGCAATTTTGCGCCAGATGCCCCTGATTTGA  2760
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2701  TGCAGGACTATCAGCGTGTTGCTGGTTCCTGCAATTTTGCGCCAGATGCCCCTGATTTGA  2760

Qy   2761  AGATCGGTTTCTTCCTCCACATTCCCTTCCCTTCCCCTGATCGTGTTCCGTCAGCTGC  2817
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2761  AGATCGGTTTCTTCCTCCACATTCCCTTCCCTTCCCCTGATCGTGTTCCGTCAGCTGC  2817
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RESULT 3
US-09-834-721-1
;  Sequence 1, Application US/0983472l
;  Patent No. US20020155551A1
;  GENERAL INFORMATION:
;  APPLICANT: RIEPING, MECHTHILD
;  TITLE OF INVENTION:  PROCESS FOR THE FERMENTATIVE PREPARATION OF L-THREONINE
;  FILE REFERENCE: 21123/280169/MAS
;  CURRENT APPLICATION NUMBER: US/09/834,721
;  CURRENT FILING DATE:  2001-04-16
;  PRIOR APPLICATION NUMBER: DE 100 26 494.8
;  PRIOR FILING DATE: 2000-05-27
;  PRIOR APPLICATION NUMBER: DE 101 02 823.7
;  PRIOR FILING DATE: 2001-01-23
;  NUMBER OF SEQ ID NOS: 12
;  SOFTWARE: PatentIn Ver. 2.1
;
;  SEQ ID NO 1
;  LENGTH: 2817
;  TYPE: DNA
;  ORGANISM: Corynebacterium glutamicum
;  FEATURE:
;  OTHER INFORMATION: ATCC14752
;  NAME/KEY: CDS
;  LOCATION: (398)..(1864)
;  OTHER INFORMATION: thrE gene
US-09-834-721-1

Query Match                       100.0%;  Score 2817;  DB 9;  Length 2817;
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Best Local Similarity 100.0%; Pred. No. 0; Gaps 0;
Matches 2817; Conservative 0; Mismatches 0; Indels 0;

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Qy     1 AATGAAATAATCCCTCACCAACTGGCACATTCAAACACCGTTCAATTCCAAACATCG   60
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Db     1 AATGAAATAATCCCTCACCAACTGGCACATTCAAACACCGTTCAATTCCAAACATCG   60

Qy    61 AGCCAAGGGAAAGAAAGCCCTAAGCCCGTGTTATTAAATGGAGACTCTTTGGAGACC  120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61 AGCCAAGGGAAAGAAAGCCCTAAGCCCGTGTTATTAAATGGAGACTCTTTGGAGACC  120

Qy   121 TCAAGCCAAAAGGGGCATTTCATTAAGAAAATACCCCTTGACCTGGTGTATTGAGC   180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 TCAAGCCAAAAGGGGCATTTCATTAAGAAAATACCCCTTGACCTGGTGTATTGAGC   180

Qy   181 TGGAGAAGAGACTTGAACTCTCAACCTACGCATTACAAGTGCGTGCCTGCCAATTGCG  240
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 TGGAGAAGAGACTTGAACTCTCAACCTACGCATTACAAGTGCGTGCCTGCCAATTGCG  240

Qy   241 CCACTCCAGCACCGCAGATGCTGATGATCAACAACTACGAATCTTAGCGTATGT  300
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 CCACTCCAGCACCGCAGATGCTGATGATCAACAACTACGAATCTTAGCGTATGT  300

Qy   301 GTACATCACAAATGAAATCGGGGCTAGAGTATCTGGTGAACCGTGCATAAACGACCTGTG  360
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 GTACATCACAAATGAAATCGGGGCTAGAGTATCTGGTGAACCGTGCATAAACGACCTGTG  360

Qy   361 ATTGGACTCTTTTTCCTTGCAAAATGTTTTCCAGCGGATGTGAGTTTTGCGACCCGTTCG  420
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Db   361 ATTGGACTCTTTTTCCTTGCAAAATGTTTTCCAGCGGATGTGAGTTTTGCGACCCGTTCG  420

Qy   421 TGGCCGCATTTCAACAGTTGACGCTGCAAAAGCCGCACCTCCGCCATCGCCACTAGCCCC  480
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 TGGCCGCATTTCAACAGTTGACGCTGCAAAAGCCGCACCTCCGCCATCGCCACTAGCCCC  480

Qy   481 GATTGATCTCACTGACCATAGTCAAGTGCCGGTGTGATGAATTGGCTGCGGAGAATTGG  540
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Db   481 GATTGATCTCACTGACCATAGTCAAGTGCCGGTGTGATGAATTGGCTGCGGAGAATTGG  540

Qy   541 CGATATTTGCTTTCTCAGGTACGTCAAACAGTGATACCAAGGTGCAAGTTCGAGCGGT  600
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Db   541 CGATATTTGCTTTCTCAGGTACGTCAAACAGTGATACCAAGGTGCAAGTTCGAGCGGT  600

Qy   601 GACCTCTGCGTATGGCCTGTACTATACGCATGTGGATATCAGTTGAATACGATCACCAT  660
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601 GACCTCTGCGTATGGCCTGTACTATACGCATGTGGATATCAGTTGAATACGATCACCAT  660

Qy   661 CTTCACCAACATCGGGTGTGGAGGAAGAGAGATGCCGGTCAACGTGTGTTCATGTGTGGGCAA  720
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   661 CTTCACCAACATCGGGTGTGGAGGAAGAGAGATGCCGGTCAACGTGTGTTCATGTGTGGGCAA  720

Qy   721 GTTGGACACCAACTTCTCCAAACTGTCTGAGGTTGACCGTTGACCGTTCATTCAGGC  780
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   721 GTTGGACACCAACTTCTCCAAACTGTCTGAGGTTGACCGTTGACCGTTCATTCAGGC  780

Qy   781 TGGTGCTACCCCGCCTGAGGTTGCCGAGAAAATTCTGACGAGTTGGAGCAATCGCCTGC  840
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   781 TGGTGCTACCCCGCCTGAGGTTGCCGAGAAAATTCTGACGAGTTGGAGCAATCGCCTGC  840

Qy   841 GTCTTATGGTTGGGTGGTGGATGGCAGGTTCCCTAATTGCTTTATTACCGCGTTCACGATCAT  900
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   841 GTCTTATGGTTGGGTGGTGGATGGCAGGTTCCCTAATTGCTTTATTACCGCGTTCACGATCAT  900

Qy   901 GCTGTTGGGGTGGTGGATGGCAGGTTCCCTAATTGCTTTATTACCGCGTTCACGATCAT  960
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Db   901 GCTGTTGGGGTGGTGGATGGCAGGTTCCCTAATTGCTTTATTACCGCGTTCACGATCAT  960

Qy   961 TGCCACGACGTCATTTTTGGGAAAGAAGGGTTTGCCTACTTTCTTCCAAAATGTTGTTGG 1020
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   961 TGCCACGACGTCATTTTTGGGAAAGAAGGGTTTGCCTACTTTCTTCCAAAATGTTGTTGG 1020

Qy  1021 TGGTTTTATTGCCACGCTGCCTGCTGCATCGATTGCTTATTCTTTGGCGTTGTGTTGGTCT 1080
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1021 TGGTTTTATTGCCACGCTGCCTGCTGCATCGATTGCTTATTCTTTGGCGTTGTGTTGGTCT 1080

Qy  1081 TGAGATCAAACCGAGCCAGATCATCGATCATCTGGAATTGTTGTCGTTGTTGGCAGGTTTGAC 1140
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1081 TGAGATCAAACCGAGCCAGATCATCGATCATCTGGAATTGTTGTCGTTGTTGGCAGGTTTGAC 1140

Qy  1141 ACTTGTGCAATCTCTGCAGGACGGCATCACAGGGCGCTCCGGTGACAGCAAGTGCACGATT 1200
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1141 ACTTGTGCAATCTCTGCAGGACGGCATCACAGGGCGCTCCGGTGACAGCAAGTGCACGATT 1200

Qy  1201 TTTTGAAACACTCCTGTTTACCGGCGGCATTGTTGCTGCGGGGTTTGGGCATTCAGCT 1260
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Db  1201 TTTTGAAACACTCCTGTTTACCGGCGGCATTGTTGCTGCGGGGTTTGGGCATTCAGCT 1260

Qy  1261 TTCTGAAATCTTGCATGTCATGTTGCTCTGCCATGAGTCCGTGCGAGCGACCTAATTATTC 1320
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1261 TTCTGAAATCTTGCATGTCATGTTGCTCTGCCATGAGTCCGTGCGAGCGACCTAATTATTC 1320

Qy  1321 GTCTACATTCGCCCCATTATCGCTGGTGCGTCACCGCGCCTTCGCAGTGGGTTG 1380
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1321 GTCTACATTCGCCCCATTATCGCTGGTGCGTCACCGCGCCTTCGCAGTGGGTTG 1380

Qy  1381 TTACGCGGAGTGGTCCTCGGTGATTATTGCGGGGCTTACTGCGCTGTATGGGTTCTGCGTT 1440
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1381 TTACGCGGAGTGGTCCTCGGTGATTATTGCGGGGCTTACTGCGCTGTATGGGTTCTGCGTT 1440

Qy  1441 TTATTACCTCTTCGGTGTGTTTATTAGGCCCGTCTCGCCGCTCTGCGCGTCTGCAACAGC 1500
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Db  1441 TTATTACCTCTTCGGTGTGTTTATTAGGCCCGTCTCGCCGCTCTGCGCGTCTGCAACAGC 1500

Qy  1501 AGTTGGTTCACTGGCGGTTGCTTGCCCGCTCGATTCTTGATTCTGATTCTCACCGGTGTGGC 1560
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1501 AGTTGGTTCACTGGCGGTTGCTTGCCCGCTCGATTCTTGATTCTGATTCTCACCGGTGTGGC 1560

Qy  1561 GATTGCCGGCATCACACCCATAACCGGTGCATTTACCGGCAATTACCGCGGAATGTACGCCAC 1620
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Db  1561 GATTGCCGGCATCACACCCATAACCGGTGCATTTACCGGCAATTACCGCGGAATGTACGCCAC 1620

Qy  1621 CTTGAATGATCAAACACTCATGGGTTTCACCAACATTGCGGTTGCTTAGCCACTGCTTC 1680
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1621 CTTGAATGATCAAACACTCATGGGTTTCACCAACATTGCGGTTGCTTAGCCACTGCTTC 1680

Qy  1681 ATCACTTGCGCTGCGCTGGCGTGGTTTGGGTGAGTGGATTGCCCGCAGGCTACGTCGTCCACC 1740
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Db  1681 ATCACTTGCGCTGCGCTGGCGTGGTTTGGGTGAGTGGATTGCCCGCAGGCTACGTCGTCCACC 1740

Qy  1741 ACGCTTCAACCCATACCGTGCAATTACCAAGGCGAATGAGTTCTCCTTCCAGGAGGAAGC 1800
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Db  1741 ACGCTTCAACCCATACCGTGCAATTACCAAGGCGAATGAGTTCTCCTTCCAGGAGGAAGC 1800

Qy  1801 TGAGCAGAATCAGCCGCCGGCAGGAATGATGCCGGTCAACAGTCAATCAAAGATTCGGTAATAA 1860
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Db  1801 TGAGCAGAATCAGCCGCCGGCAGGAATGATGCCGGTCAACAGTCAATCAAAGATTCGGTAATAA 1860

Qy  1861 AAGGTAAAAATCAACCGTGCAATTCTGACGAGTTGGAGCAATCGGGTCGA 1920
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Db  1861 AAGGTAAAAATCAACCGTGCAATTCTGACGAGTTGGAGCAATCGGGTCGA 1920

Qy  1921 TCGCTTTTAAACTCAGGATCCTTGCCGGCCAAAATCACGGACACTCGTCCCACCC 1980
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Db  1921 TCGCTTTTAAACTCAGGATCCTTGCCGGCCAAAATCACGGACACTCGTCCCACCC 1980

Qy  1981 CAGAATCCCTCACGCTGTTGAAGAGGAACCGCAGGAATTGTTGCCA 2040
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Db  1981 CAGAATCCCTCACGCTGTTGAAGAGGAACCGCAGGAATTGTTGCCA 2040

Qy  2041 CCTATTCTCAAGGACTTCTTCGACGCGTCACTTTGATGTGCATGCTCGGCGTTGAACCTCGA 2100
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2041 CCTATTCTCAAGGACTTCTTCGACGCGTCACTTTGATGTGCATGCTCGGCGTTGAACCTC 2100

Qy  2101 AGGGCCTGCGTTACACCAAGGTCGCTTCTGAAACGAGAACGAGGAAGCTCAGCCAAAGAAGGCTA 2160
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2101 AGGGCCTGCGTTACACCAAGGTCGCTTCTGAAACGAGAACGAGGAAGCTCAGCCAAAGAAGGCTA 2160
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Best Local Similarity   100.0%; Pred. No. 0;
Matches 2817; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

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Qy      1 AATGAAATAATCCCTCACCAACTGGCACATTCAAACACCGTTCATTCAAACATCG    60
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Db      1 AATGAAATAATCCCTCACCAACTGGCACATTCAAACACCGTTCATTCAAACATCG    60

Qy     61 AGCCAAGGGAAAGAGAAGCCCCTAAGCCCGTGTTATTAAATGGAGACTCTTTGGAGACC   120
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Db     61 AGCCAAGGGAAAGAGAAGCCCCTAAGCCCGTGTTATTAAATGGAGACTCTTTGGAGACC   120

Qy    121 TCAAGCCAAAAGGGGCATTTCATTAAGAAAATACCCCTTGACCTGTGTGTTATTGAGC   180
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Db    121 TCAAGCCAAAAGGGGCATTTCATTAAGAAAATACCCCTTGACCTGTGTGTTATTGAGC   180

Qy    181 TGGAGAAGAGACTTGAACTCTCAACCTACGCATTACAAGTGCGTTGCCTGCCAATTGCG   240
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Db    181 TGGAGAAGAGACTTGAACTCTCAACCTACGCATTACAAGTGCGTTGCCTGCCAATTGCG   240

Qy    241 CCACTCCAGCACCCGAGTGCTGATGATCAACAACTACGAATACGTATCTTAGCGTATGT   300
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Db    241 CCACTCCAGCACCCGAGTGCTGATGATCAACAACTACGAATACGTATCTTAGCGTATGT   300

Qy    301 GTAATCACAAATGGAATTCGGGGCTAGAGTATCTGGTGAACCGTGCATAAACGACCTGTG   360
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Db    301 GTAATCACAAATGGAATTCGGGGCTAGAGTATCTGGTGAACCGTGCATAAACGACCTGTG   360

Qy    361 ATTGGACTCTTTTCCTTGCAAAATGTTTCCAGCGGATGTGAGTTTTGCGACCCCTTCG   420
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Db    361 ATTGGACTCTTTTCCTTGCAAAATGTTTCCAGCGGATGTGAGTTTTGCGACCCCTTCG   420

Qy    421 TGGCCGCATTTCAACAGTTGACGCTGCAAAAGCCGCACCTCCGCCATCGCCACTAGCCCC   480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 TGGCCGCATTTCAACAGTTGACGCTGCAAAAGCCGCACCTCCGCCATCGCCACTAGCCCC   480

Qy    481 GATTGATCTCACTGACCATAGTCAAGTGGCCGGTGTGATGAATTGGCTGCGAGAATTGG   540
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Db    481 GATTGATCTCACTGACCATAGTCAAGTGGCCGGTGTGATGAATTGGCTGCGAGAATTGG   540

Qy    541 CGATATTTGCTTTCTTCAGGTACGTCAAACAGTGATACCAAGGTGCAAGTTCGAGCGGT   600
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 CGATATTTGCTTTCTTCAGGTACGTCAAACAGTGATACCAAGGTGCAAGTTCGAGCGGT   600

Qy    601 GACCTCTGCGTATGGCCTGTACTATACGCATGTGGATATCACGTTGAATACGATCACCAT   660
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 GACCTCTGCGTATGGCCTGTACTATACGCATGTGGATATCACGTTGAATACGATCACCAT   660

Qy    661 CTTCACCAACATCGGTTGTGAGGAGAAGATGCCGGTCAACGTTCATGTTGTGGGCAA   720
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Db    661 CTTCACCAACATCGGTTGTGAGGAGAAGATGCCGGTCAACGTTCATGTTGTGGGCAA   720

Qy    721 GTTGGACACCAACTTCTCCAAACTGTCTGAGGTTGACCGGTTGATCCGTTCCATTCAGGC   780
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Qy    781 TGGTGCTACCCCGCCTGAGGTTGCCGGAGAAATTCTGGACGAGTTGGAGCAATCGGCTGC   840
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Db    781 TGGTGCTACCCCGCCTGAGGTTGCCGGAGAAATTCTGGACGAGTTGGAGCAATCGGCTGC   840

Qy    841 GTCTTATGGTTTCCCGTTGCGTTGCGTTTGGGCAATGATGGGGCGCTGTTGCTGT   900
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Db    841 GTCTTATGGTTTCCCGTTGCGTTGCGTTTGGGCAATGATGGGGCGCTGTTGCTGT   900

Qy    901 GCTGTTGGGTGGTGATGGCAGGTTCCCTAATTGCTTTTATTACCGGTTCACGATCAT   960
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Db    901 GCTGTTGGGTGGTGATGGCAGGTTCCCTAATTGCTTTTATTACCGGTTCACGATCAT   960

Qy    961 TGCCACGACGTCATTTTGGGAAAGAGGGTTGCCTACTTCTTCCAAAATGTTGTTGG   1020
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Db    961 TGCCACGACGTCATTTTGGGAAAGAGGGTTGCCTACTTCTTCCAAAATGTTGTTGG   1020

Qy   1021 TGGTTTATTGCCACGCTGCCGATTGCTTATTCTTTTGGGTTGCAATTTGGTCT   1080
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Qy   2161 CAAAGCGGACTCGTAAGGCACCAGCTAAGAAGGCTGCTGCTAAGAAAACGACCAAGAAGA   2220
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Db   2161 CAAAGCGGACTCGTAAGGCACCAGCTAAGAAGGCTGCTGCTAAGAAAACGACCAAGAAGA   2220

Qy   2221 CCACTAAGAAAACTACTAAAAGACCACCGCCGAAAGAGAGACCACAAAGAGAGTCTTAAGCCG   2280
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Db   2221 CCACTAAGAAAACTACTAAAAGACCACCGCCGAAAGAGAGACCACAAAGAGAGTCTTAAGCCG   2280

Qy   2281 GATCTTATATGATGATTCCAATAGCTTTGTAGTTGTTGCTAACCGTCTCGCCAGTGGATA   2340
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Db   2281 GATCTTATATGATGATTCCAATAGCTTTGTAGTTGTTGCTAACCGTCTGCCAGTGGATA   2340

Qy   2341 TGACTGTCCACCGATGGTAGCTATAGCATCTCCCCAGCCCCGGTGGCCTTGTCACGG   2400
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Db   2341 TGACTGTCCACCGATGGTAGCTATAGCATCTCCCCAGCCCCGGTGGCCTTGTCACGG   2400

Qy   2401 GGCTTTCCCCGTTCCGGACAACAATCGTGGGTCGGATGGCCTGGAACTGTAG   2460
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Qy   2461 ATGTTGCACCCGAACCATTTCGAACAGATACGGGTGTTTTGCTGCGCAACGTGTGTCCTCA   2520
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Qy   2521 CTGCAAGTGACTATGAAGGCTTCTACGAGGGCTTTCAAACGCAACGTGGTGCATGCGTTTCG   2580
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy   2581 TCCACGATTGATTGTTACTCCGGTGTACACACCGATTGGTGCGGCATCGGTTTCGGGAAG   2640
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Db   2581 TCCACGATTGATTGTTACTCCGGTGTACACACCGATTGGTGCGGCATCGGTTTCGGGAAG   2640

Qy   2641 TAAACCTCAAGTTCGCTGAAGCCGTGAGCCAAGTGGCGGCACACGTGCCACTGTGTGGG   2700
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Qy   2701 TGCAGGACTATCAGCTGTTGCTGGTTCCTGGCATTTGCGCCAGATGCGCCCTGATTTGA   2760
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Db   2701 TGCAGGACTATCAGCTGTTGCTGGTTCCTGGCATTTGCGCCAGATGCGCCCTGATTTGA   2760

Qy   2761 AGATCGGTTTCTTCCTCCACATTCCCTTCCCTCCCCTGATCTGTTCCGTCAGCTGC   2817
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RESULT 4
US-09-783-388-1
; Sequence 1, Application US/09783388
; Patent No. US2002016873lA1
; GENERAL INFORMATION:
; APPLICANT: Ziegler, Petra
; APPLICANT: Eggeling, Lothar
; APPLICANT: Sahm, Hermann
; APPLICANT: Thierbach, Georg
; TITLE OF INVENTION: NEW NUCLEOTIDE SEQUENCES CODING FOR THE THRE GENE AND
; TITLE OF INVENTION: PROCESS FOR
; TITLE OF INVENTION: ENZYMATIC PRODUCTION OF L-THREONINE USING CORYNEFORM BACTERIA
; FILE REFERENCE: 21123/277066
; CURRENT APPLICATION NUMBER: US/09/783,388
; CURRENT FILING DATE: 2001-02-15
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.0
;
; SEQ ID NO 1
; LENGTH: 2817
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum ATCC14752
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (398)..(1864)
US-09-783-388-1

Query Match   100.0%; Score 2817; DB 9; Length 2817;

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Db   1021  TGGTTTTATTGCCACGCTGCCTGCCATCGATTGCTTATTCTTTGGCGTTGCAATTTGGTCT  1080

Qy   1081  TGAGATCAAACCGAGCCAGATCATCGCATCTGGAATTGTTGTGCTGTTGGCAGGTTTGAC  1140
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Db   1081  TGAGATCAAACCGAGCCAGATCATCGCATCTGGAATTGTTGTGCTGTTGGCAGGTTTGAC  1140

Qy   1141  ACTTGTGCAATCTCTGCAGGACGGCATCACGGGCGCTCCGGTGCAGCAAGTGCACGATT   1200
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Qy   1201  TTTTGAAACACTTCCTGTTTACCGGCATTGTTGCTGGCGTGGGTTTGGGCATTCAGCT    1260
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Qy   1261  TTCTGAAATCTTGCATGTCATGTGCCATGGAGTCCGCTGCAGCACCTAATTATTC       1320
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Qy   1321  GTCTACAATTCGCCCGCATTATCCGTGGTGGCCTTCGCCAGCGGCCTTCGCCAGTGGGTTG 1380
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Qy   1381  TTACGCGGAGTGTCCTCGGTGATTATTGCGGGGCTTACTGCGCTGATGGGTTCTGCGTT   1440
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Db   1381  TTACGCGGAGTGTCCTCGGTGATTATTGCGGGGCTTACTGCGCTGATGGGTTCTGCGTT   1440

Qy   1441  TTATTACCTCTCTCGTTGTTTATTAGGCCCCGTCTCTCGCCGCTGCGATTGCTGCAACAGC 1500
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Qy   1501  AGTTGGTTTCACTGGTGGTTGCTTGCCCGTCGATTCCGTTGATTCCACCGTTGATTGTGGC 1560
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1501  AGTTGGTTTCACTGGTGGTTGCTTGCCCGTCGATTCCGTTGATTCCACCGTTGATTGTGGC 1560

Qy   1561  GATTGCCGGCATCACACCAAATGCTTCCAGGTTCTAGCAATTTACCGCGGAATGTACGCCAC 1620
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Db   1561  GATTGCCGGCATCACACCAAATGCTTCCAGGTTCTAGCAATTTACCGCGGAATGTACGCCAC 1620

Qy   1621  CTTGAATGATCAAACACTCATGGGTTCACCACAACACTTGCGGTTGCTTTAGCCACTGCTTC 1680
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Db   1621  CTTGAATGATCAAACACTCATGGGTTCACCACAACACTTGCGGTTGCTTTAGCCACTGCTTC 1680

Qy   1681  ATCACTTGCCGCTGGCGTGGTTTGGGTGAGTGGATTGCCCGGCTACGTCGTCCACC      1740
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Db   1681  ATCACTTGCCGCTGGCGTGGTTTGGGTGAGTGGATTGCCCGGCTACGTCGTCCACC      1740

Qy   1741  ACGCTTCAACCGTGCATTACCAAGGCGAATGAGTTCTCCTTCCAGGAGGAAGC         1800
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Db   1741  ACGCTTCAACCGTGCATTACCAAGGCGAATGAGTTCTCCTTCCAGGAGGAAGC         1800

Qy   1801  TGAGCAGAATCAGCGCCGGCAGAGAAAACGTCCAAGACTAATCAAAGATTCGGTAATAA   1860
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Db   1801  TGAGCAGAATCAGCGCCGGCAGAGAAAACGTCCAAGACTAATCAAAGATTCGGTAATAA   1860

Qy   1861  AAGGTAAAAATCAACCTCTTTCGCTTAAATAGCGTAGAATATCGGGTCGA             1920
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Db   1861  AAGGTAAAAATCAACCTCTTTCGCTTAAATAGCGTAGAATATCGGGTCGA             1920

Qy   1921  TCGCTTTAAACACTCAGGAGATCCTTGCCGGCCAAAATCACGGACACTCGTCCCACCC     1980
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Db   1921  TCGCTTTAAACACTCAGGAGATCCTTGCCGGCCAAAATCACGGACACTCGTCCCACCC     1980

Qy   1981  CAGAATCCCTTCACGCGTGTTGAAGAGGAAAACCGCAGCCGGTCCCCGGATTGTTGCCA   2040
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1981  CAGAATCCCTTCACGCGTGTTGAAGAGGAAAACCGCAGCCGGTCCCCGGATTGTTGCCA   2040

Qy   2041  CCTATTCTAAGGACTTCTTCGACGCGCTCACTTTGAATGTGCATGCGGTTCGGCGTTGAACCTC 2100
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2041  CCTATTCTAAGGACTTCTTCGACGCGCTCACTTTGAATGTGCATGCGGTTCGGCGTTGAACCTC 2100

Qy   2101  AGGGCCTGCGTTACACCAAGGTCGCTTCGCTTCTGAACACGGAAGCTCAGCCAAAGAAGCTA 2160
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2101  AGGGCCTGCGTTACACCAAGGTCGCTTCGCTTCTGAACACGGAAGCTCAGCCAAAGAAGCTA 2160
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Qy   2161  CAAAGCCGGACTCGTAAGGCACCAGCTAAGAAAGGCTGCTCGTGAAGAAAACGACCAAGAAGA  2220
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2161  CAAAGCCGGACTCGTAAGGCACCAGCTAAGAAAGGCTGCTCGTGAAGAAAACGACCAAGAAGA  2220

Qy   2221  CCACTAAGAAAACTACTAAAAAGACCACCGCCAAAGAAGACCACAAAGAAGAGTCTTAAGCCG  2280
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2221  CCACTAAGAAAACTACTAAAAAGACCACCGCCAAAGAAGACCACAAAGAAGAGTCTTAAGCCG  2280

Qy   2281  GATCTTATATGATGATTCCAATAGCTTTGTAGTTGTTGTGCTAACCGTCTCGCCAGTGGATA  2340
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2281  GATCTTATATGATGATTCCAATAGCTTTGTAGTTGTTGTGCTAACCGTCTCGCCAGTGGATA  2340

Qy   2341  TGACTGTCCACCCAGATGGTAGCTATAGCATCTCCCCAGCCCCGGTCGCCTTGTCACGG     2400
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2341  TGACTGTCCACCCAGATGGTAGCTATAGCATCTCCCCAGCCCCGGTCGCCTTGTCACGG     2400

Qy   2401  GGCTTCCCCGTTCTCGGAACAACATCGTGGGTCGGATGGCCGGATGGCCTGGAACTGTAG    2460
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2401  GGCTTCCCCGTTCTCGGAACAACATCGTGGGTCGGATGGCCGGATGGCCTGGAACTGTAG    2460

Qy   2461  ATGTTGCACCGAACCATTTCGAACAGATACGGGTGTTTTCTGCACCCGTGTGTCCTCA      2520
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2461  ATGTTGCACCGAACCATTTCGAACAGATACGGGTGTTTTCTGCACCCGTGTGTCCTCA      2520

Qy   2521  CTGCAAGTGACTATGAAGGCTTCTACGAGGGCTTTTCAAACGCACGCGTGTGGCCTCTTT    2580
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2521  CTGCAAGTGACTATGAAGGCTTCTACGAGGGCTTTTCAAACGCACGCGTGTGGCCTCTTT    2580

Qy   2581  TCCACGATTTGATTGTTACTCCGGTGTACAACACCGATTGGTGGCATGCGTTTCGGGAAG    2640
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2581  TCCACGATTTGATTGTTACTCCGGTGTACAACACCGATTGGTGGCATGCGTTTCGGGAAG    2640

Qy   2641  TAAACCTCAAGTTCGCTGAAGCCGTGAGCCAAGTGGCGGCACACGGTGCCACTGTGTGGG   2700
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2641  TAAACCTCAAGTTCGCTGAAGCCGTGAGCCAAGTGGCGGCACACGGTGCCACTGTGTGGG   2700

Qy   2701  TGCAGGACTATCAGCTGTTGCTCGTTCCTGGCATTTTGGCGCCAGATGCGCCCTGATTTGA  2760
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2701  TGCAGGACTATCAGCTGTTGCTCGTTCCTGGCATTTTGGCGCCAGATGCGCCCTGATTTGA  2760

Qy   2761  AGATCGGTTTCTTCCTCCTCCACATTCCCCTTCCCTTCCCCTTCCCTGATCTGTTCCGTCAGCTGC  2817
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2761  AGATCGGTTTCTTCCTCCTCCACATTCCCCTTCCCTTCCCCTTCCCTGATCTGTTCCGTCAGCTGC  2817
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RESULT 5
US-09-951-535-1
; Sequence 1, Application US/09951535
; Publication No. US20030049802A1
; GENERAL INFORMATION:
;   APPLICANT: ZIEGLER, PETRA
;   APPLICANT: EGGELING, LOTHAR
;   APPLICANT: SAHM, HERMANN
;   APPLICANT: THIERBACH, GEORG
;   TITLE OF INVENTION: NEW NUCLEOTIDE SEQUENCES CODING FOR THE THRE GENE AND
;   TITLE OF INVENTION: PROCESS FOR THE ENZYMATIC PRODUCTION OF L-THREONINE
;   TITLE OF INVENTION: USING CORYNEFORM BACTERIA
;   FILE REFERENCE: 21123/282415/MAS
;   CURRENT APPLICATION NUMBER: US/09/951,535
;   CURRENT FILING DATE: 2001-09-14
;   PRIOR APPLICATION NUMBER: 09/431,099
;   PRIOR FILING DATE: 1999-11-01
;   PRIOR APPLICATION NUMBER: DE 199 41 478.5
;   PRIOR FILING DATE: 1999-09-01
;   NUMBER OF SEQ ID NOS: 10
;   SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
;   LENGTH: 2817
;   TYPE: DNA
;   ORGANISM: Corynebacterium glutamicum
;   FEATURE:
;   NAME/KEY: CDS

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;  LOCATION: (398)..(1864)
;  OTHER INFORMATION: thrB-Gen
US-09-951-535-1

Query Match        100.0%;  Score 2817;  DB 10;  Length 2817;
Best Local Similarity  100.0%;  Pred. No. 0;
Matches 2817;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy      1 AATGAAATAATCCCCTCACCAACTGCGACATTCAAACACCGTTCATTCCAAACATCG    60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 AATGAAATAATCCCCTCACCAACTGCGACATTCAAACACCGTTCATTCCAAACATCG    60

Qy     61 AGCCAAGGGAAAAGAAAGCCCTAGCCCGTGTTATTAAATGGAGACTCTTTGGAGACC   120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 AGCCAAGGGAAAAGAAAGCCCTAGCCCGTGTTATTAAATGGAGACTCTTTGGAGACC   120

Qy    121 TCAAGCCAAAAGGGGCATTTCATTAAGAAAATACCCCTTTGACCTGGTGTTATTGAGC   180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 TCAAGCCAAAAGGGGCATTTCATTAAGAAAATACCCCTTTGACCTGGTGTTATTGAGC   180

Qy    181 TGGAGAAGAGACTTGAACTCTCAACCTACGCATTACAGAGTGCGTTGCCGCTGCCAATTGCG   240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 TGGAGAAGAGACTTGAACTCTCAACCTACGCATTACAGAGTGCGTTGCCGCTGCCAATTGCG   240

Qy    241 CCACTCCAGCACCGCAGATGCTGATGATCAACAACTACGAATACGTATCTTAGCGTATGT   300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 CCACTCCAGCACCGCAGATGCTGATGATCAACAACTACGAATACGTATCTTAGCGTATGT   300

Qy    301 GTACATCACAATGGAATTCGGGGCTAGAGTATCTGGTGAACCGTGCATAAACGACCTGTG   360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 GTACATCACAATGGAATTCGGGGCTAGAGTATCTGGTGAACCGTGCATAAACGACCTGTG   360

Qy    361 ATTGGACTTCTTTTCCTTGCAAAATGTTTCCAGCGATGTTGAGTTGAGTTTTGCGACCCTTCG   420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 ATTGGACTTCTTTTCCTTGCAAAATGTTTCCAGCGATGTTGAGTTGAGTTTTGCGACCCTTCG   420

Qy    421 TGGCCGCATTTCAACAGTTGACGCTGCAAAAGCCGCACCTCCGCCATCGCCACTAGCGCC   480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 TGGCCGCATTTCAACAGTTGACGCTGCAAAAGCCGCACCTCCGCCATCGCCACTAGCGCC   480

Qy    481 GATTGATCTCACTGACCATAGTCAAGTGCCGGTGTGATGAATTGGCTGCCGAGAATTGG   540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 GATTGATCTCACTGACCATAGTCAAGTGCCGGTGTGATGAATTGGCTGCCGAGAATTGG   540

Qy    541 CGATATTTTGCTTTCTTCAGGTACGTCAAACAGTGATACCAAGGTGCAAGTTCGAGCGGT   600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 CGATATTTTGCTTTCTTCAGGTACGTCAAACAGTGATACCAAGGTGCAAGTTCGAGCGGT   600

Qy    601 GACCTCTGCGTATGGCCTGTATCTATACGTGGATATCACGTTGAATACGGATCACCAT   660
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 GACCTCTGCGTATGGCCTGTATCTATACGTGGATATCACGTTGAATACGGATCACCAT   660

Qy    661 CTTCACCAACAACATCGGTGTGGAGGAGAGATGCCGGTCAAGGCGGTTGTCCTTCATGTTGTTGGGCAA   720
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 CTTCACCAACAACATCGGTGTGGAGGAGAGATGCCGGTCAAGGCGGTTGTCCTTCATGTTGTTGGGCAA   720

Qy    721 GTTGGACACCAACTTCTCCAAATGTCTGAGGTTGCCGAGAAATTCTGACGAGTTGGAGCAATCGCCTGC   780
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 GTTGGACACCAACTTCTCCAAATGTCTGAGGTTGCCGAGAAATTCTGACGAGTTGGAGCAATCGCCTGC   780

Qy    781 TGGTGCTACCCCGCCTGAGGTTTCCCTGTTGCCTGGCTGGCAATGGGTGGCCTGTGTTGCTGT   840
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 TGGTGCTACCCCGCCTGAGGTTTCCCTGTTGCCTGGCTGGCAATGGGTGGCCTGTGTTGCTGT   840

Qy    841 GTCTTATGTGTTTGCCCTGTTGGATGGCAGGTTTCCGGTTCACGGTTCACGATCAT   900
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 GTCTTATGTGTTTGCCCTGTTGGATGGCAGGTTTCCGGTTCACGGTTCACGATCAT   900

Qy    901 GCTGTTGGGTGTGGATGGCAGAGTTTCCCTAATTGCTTTTATTACCGGTTCACGATCAT   960
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 GCTGTTGGGTGTGGATGGCAGAGTTTCCCTAATTGCTTTTATTACCGGTTCACGATCAT   960

Qy    961 TGCCACGACGTCATTTTGGGAAAGAAGAGGGTTTGCCTACTTTCTTCCAAATGTGTTGTTGG  1020
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961 TGCCACGACGTCATTTTGGGAAAGAAGAGGGTTTGCCTACTTTCTTCCAAATGTGTTGTTGG  1020

Qy   1021 TGGTTTTATTGCCACGCTGCCTGCATCGATTGCTTATTCTTCTTGGCGTTGCAATTGGTCT  1080
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 TGGTTTTATTGCCACGCTGCCTGCATCGATTGCTTATTCTTCTTGGCGTTGCAATTGGTCT  1080

Qy   1081 TGAGATCAAACCGAGCCAGATCATCGCATCTGAATTGTGTCGTGTTGGCAGTTTGAC  1140
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 TGAGATCAAACCGAGCCAGATCATCGCATCTGAATTGTGTCGTGTTGGCAGTTTGAC  1140

Qy   1141 ACTTGTGCAATCTCTGCAGGACGGCATCACGGGCGCTCCGGTGACAGCAAGTGCACGATT  1200
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141 ACTTGTGCAATCTCTGCAGGACGGCATCACGGGCGCTCCGGTGACAGCAAGTGCACGATT  1200

Qy   1201 TTTTGAAACACTCCTGTTTACCGGCGGCATTGTTGCTGGCGGCATTGTTGGGGTTGGGCATTCAGCT  1260
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1201 TTTTGAAACACTCCTGTTTACCGGCGGCATTGTTGCTGGCGGCATTGTTGGGGTTGGGCATTCAGCT  1260

Qy   1261 TTCTGAAATCTTGCATGTCATGTGCCATGCCGTCGCTGCAGCACCTTAATTATTC  1320
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1261 TTCTGAAATCTTGCATGTCATGTGCCATGCCGTCGCTGCAGCACCTTAATTATTC  1320

Qy   1321 GTCTACATTCGCCCGCATTATGCTGGTGCGCCGCACCGCAGGCGGCCTTCGCGAGTGGGGTG  1380
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1321 GTCTACATTCGCCCGCATTATGCTGGTGCGCCGCACCGCAGGCGGCCTTCGCGAGTGGGGTG  1380

Qy   1381 TTACGCGGAGTGGTGCTCCTGGTGATTATTGTAGGCCCCGCTTACTGCGCTTACTGGTTCTGCGTT  1440
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1381 TTACGCGGAGTGGTGCTCCTGGTGATTATTGTAGGCCCCGCTTACTGCGCTTACTGGTTCTGCGTT  1440

Qy   1441 TTATTACCCTTCGTGTGTTATTGTTGTTTATTTAGGCCCGCTCTCGCGCCTGCGATTCTTGATTCCACCGGTTGATTGTGGC  1500
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1441 TTATTACCCTTCGTGTGTTATTGTTGTTTATTTAGGCCCGCTCTCGCGCCTGCGATTCTTGATTCCACCGGTTGATTGTGGC  1500

Qy   1501 AGTTGGTTTCACTGGTGGTTTGCTTGCCCGTCGATTCTTGATTCCACCGGTTGATTGTGGC  1560
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1501 AGTTGGTTTCACTGGTGGTTTGCTTGCCCGTCGATTCTTGATTCCACCGGTTGATTGTGGC  1560

Qy   1561 GATTGCCGGCATCACACCAAGTGCTTCCAGGTCTAGCAATTTACCGCGGAATGTACGCCAC  1620
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1561 GATTGCCGGCATCACACCAAGTGCTTCCAGGTCTAGCAATTTACCGCGGAATGTACGCCAC  1620

Qy   1621 CTTGAATGATCATCAAACACTCATGGGTTCACCAAGTTGCGGTTGCTTTAGCCACTGCTTC  1680
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1621 CTTGAATGATCATCAAACACTCATGGGTTCACCAAGTTGCGGTTGCTTTAGCCACTGCTTC  1680

Qy   1681 ATCACTTGCCGCTGGCGTGTTTTGGGTGAGTGAGTTGGGTGAGTGAGTTGCCCAGGCTACGTCGTCCACC  1740
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1681 ATCACTTGCCGCTGGCGTGTTTTGGGTGAGTGAGTTGGGTGAGTGAGTTGCCCAGGCTACGTCGTCCACC  1740

Qy   1741 ACGCTTCAACCCATACGTGCATTACCAAGGCGGAATGGAGTTCTCTTCCAGGAGGAAGC  1800
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1741 ACGCTTCAACCCATACGTGCATTACCAAGGCGGAATGGAGTTCTCTTCCAGGAGGAAGC  1800

Qy   1801 TGAGCAGAATCAGCGCCGGCGAGAAAACGTCCAAAGACTAATCAACAGATTCGGTAATAA  1860
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1801 TGAGCAGAATCAGCGCCGGCGAGAAAACGTCCAAAGACTAATCAACAGATTCGGTAATAA  1860

Qy   1861 AAGGTAAAAATCAACCTGCTTCGCTTAAATAGCGTAGAATATCGGGTCCCACCTGCTGA  1920
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1861 AAGGTAAAAATCAACCTGCTTCGCTTAAATAGCGTAGAATATCGGGTCCCACCTGCTGA  1920

Qy   1921 TCGCTTTAAACACTCAGGAGATCCTTCGCGTTGCCGGCCAAATCACCGGACACTCGTTCCACCC  1980
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1921 TCGCTTTAAACACTCAGGAGATCCTTCGCGTTGCCGGCCAAATCACCGGACACTCGTTCCACCC  1980

Qy   1981 CAGAATCCCTTCACGCTGTTGAAGAGAAACCGCAGCCCGGCTCCGGCAGGATTGTTGCCA  2040
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1981 CAGAATCCCTTCACGCTGTTGAAGAGAAACCGCAGCCCGGCTCCGGCAGGATTGTTGCCA  2040

Qy   2041 CCTATTCTAAGGACTTCTTCGACGGCGTCACTTGTGATGTGCATGCGCGGTTGAACCTC  2100
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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; OTHER INFORMATION: thr E (Threonin-exportcarrier)
US-10-224-574-9

Query Match   100.0%; Score 2817; DB 17; Length 2817;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2817; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy     1 AATGAAATAATCCCTCACCAACTGGCACATTCAAACACCGTTCATTTCAAACATCG 60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1 AATGAAATAATCCCTCACCAACTGGCACATTCAAACACCGTTCATTTCAAACATCG 60

Qy    61 AGCCAAGGGAAAAGAAAGCCCTAAGCCCGTGTTATTAAATGGAGACTCTTTGGAGACC 120
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61 AGCCAAGGGAAAAGAAAGCCCTAAGCCCGTGTTATTAAATGGAGACTCTTTGGAGACC 120

Qy   121 TCAAGCCAAAAAGGGGCATTTTCATTAAGAAAATAACCCCTTTGACCTGGTGTTATTGAGC 180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 TCAAGCCAAAAAGGGGCATTTTCATTAAGAAAATAACCCCTTTGACCTGGTGTTATTGAGC 180

Qy   181 TGGAGAAGAGACTTGAACTCTCAACCTACGCATTACAAGTGCGTTGCGCTGCCAATTGCG 240
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 TGGAGAAGAGACTTGAACTCTCAACCTACGCATTACAAGTGCGTTGCGCTGCCAATTGCG 240

Qy   241 CCACTCCAGCACCGCAGATGCTGATGATCAACAACTACGAATACGTATCTTAGCGTATGT 300
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 CCACTCCAGCACCGCAGATGCTGATGATCAACAACTACGAATACGTATCTTAGCGTATGT 300

Qy   301 GTACATCACAATGGAATTCGGGGCTAGAGTATCGGTGAACCGTGCATAAACGACCTGTG 360
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 GTACATCACAATGGAATTCGGGGCTAGAGTATCGGTGAACCGTGCATAAACGACCTGTG 360

Qy   361 ATTGGACTCTTTTCCTTGCAAAATGTTTCCAGCGGATGTTGAGTTTTGCGACCCTTCG 420
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 ATTGGACTCTTTTCCTTGCAAAATGTTTCCAGCGGATGTTGAGTTTTGCGACCCTTCG 420

Qy   421 TGGCCGCATTTCAACAGTTGACGCTGCAAAAGCCGCACCTCCGCCACTAGCCCC 480
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 TGGCCGCATTTCAACAGTTGACGCTGCAAAAGCCGCACCTCCGCCACTAGCCCC 480

Qy   481 GATTGATCTCACTGACCATAGTCAAGTGCCGTGTGATGAATTGGCTGCGAGAATTGG 540
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 GATTGATCTCACTGACCATAGTCAAGTGCCGTGTGATGAATTGGCTGCGAGAATTCG 540

Qy   541 CGATATTTTGCTTTCTTCAGGTACGTCAAACAGTGATACCAAGTGCAAGTTCGAGCGGT 600
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541 CGATATTTTGCTTTCTTCAGGTACGTCAAACAGTGATACCAAGTGCAAGTTCGAGCGGT 600

Qy   601 GACCTCTGCGTATGGCCTGTACTATACGCATGGTGGATATCACGTTGAATACGATCACCAT 660
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601 GACCTCTGCGTATGGCCTGTACTATACGCATGGTGGATATCACGTTGAATACGATCACCAT 660

Qy   661 CTTCACCAACATCGGTGTGGAGGAAGAGGAAGAGAAGTGCCGGTCAACGTGTTTCATGTGTTGTGGGCAA 720
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   661 CTTCACCAACATCGGTGTGGAGGAAGAGGAAGAGAAGTGCCGGTCAACGTGTTTCATGTGTTGTGGGCAA 720

Qy   721 GTTGGACACCAACTTCTCCAAACTGTCTGAGGTTGACCGTTCCATTCAGC 780
         |||||||||||||||||||||||||||||||||||||||||||||||||
Db   721 GTTGGACACCAACTTCTCCAAACTGTCTGAGGTTGACCGTTCCATTCAGC 780

Qy   781 TGGTGCTACCCCGCCTGAGGTTGCCGGAGCAAAAATTCTGGACGAGTTGAGCAATGCCTGC 840
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   781 TGGTGCTACCCCGCCTGAGGTTGCCGGAGAAAAATTCTGGACGAGTGGAGCAATGCCTGC 840

Qy   841 GTCTTATGGTTTCCGTGTTGCTTGGCTGGGCAATGATGGGTGGCGCTGTTGCTGT 900
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   841 GTCTTATGGTTTCCGTGTTGCTTGGCTGGGCAATGATGGGTGGCGCTGTTGCTGT 900

Qy   901 GCTGTTGGGTGGTGGATGGCAGGTTTCCCTAATTGCTTTTATTACCGCGTTCACGATCAT 960
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   901 GCTGTTGGGTGGTGGATGGCAGGTTTCCCTAATTGCTTTTATTACCGCGTTCACGATCAT 960

Qy   961 TGCCACGACGTCATTTTGGGAAAGAAGGGTTTGCCTCACTTTCTTCCAAAATGTTGTTCG 1020
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(Second column — continuing alignment, positions 2041–2817)

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Db  2041 CCTATTCTAAGGACTTCTTGACGACGGCGTCACTTTGATGTGCATGCTCGGCGTTGAACCTC 2100
Qy  2101 AGGGCCTGCGTTACACCAAGGTCGCTTCTGAACACGAGGAAGCTCAGCCAAAGAAGGCTA 2160
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2101 AGGGCCTGCGTTACACCAAGGTCGCTTCTGAACACGAGGAAGCTCAGCCAAAGAAGGCTA 2160

Qy  2161 CAAAGCCGACTCGTAAGGCACCAGCTAAGGAGCACGCTGCTGCTAAGAAAACAGCAAGAGAGA 2220
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2161 CAAAGCCGACTCGTAAGGCACCAGCTAAGGAGCACGCTGCTGCTAAGAAAACGACCAAGAAGA 2220

Qy  2221 CCACTAAGAAAACTACTAAAAAGACCACCGCAAAGAAGACCACAAGAAGAGTCTTAAGCCG 2280
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2221 CCACTAAGAAAACTACTAAAAAGACCACCGCAAAGAAGACCACAAGAAGTCTTAAGCCG 2280

Qy  2281 GATCTTATATGATGATTCCAATAGCTTTGTAGTTGTTGCTAACCGTCTCGCCAGTGATA 2340
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2281 GATCTTATATGATGATTCCAATAGCTTTGTAGTTGTTGCTAACCGTCTCGCCAGTGATA 2340

Qy  2341 TGACTGTCCACCCAGATGGTAGCTATPAGCATCTCCCCAGCCCCGGTGGCCTTGTCACGG 2400
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2341 TGACTGTCCACCCAGATGGTAGCTATAGCATCTCCCCAGCCCCGGTGGCCTTGTCACGG 2400

Qy  2401 GGCTTTCCCCGTTCTGGAACAACATCGTGGATGGTCGGATGGCCTGGAACTGTAG 2460
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2401 GGCTTTCCCCGTTCTGGAACAACATCGTGGATGGTCGGATGGCCTGGAACTGTAG 2460

Qy  2461 ATGTTGCACCGCAACCATTTGGAACAGATCGGGTGTGTTTTGCTGCACCCTGTGTCCTCA 2520
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2461 ATGTTGCACCGCAACCATTTGGAACAGATACGGGTGTGTTTTGCTGCACCCTGTGTCCTCA 2520

Qy  2521 CTGCAAGTGACTATGAGAGGCTTCTACCGAGGGCTTTCAAACGCAACCGTGTGGCCTCTTT 2580
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2521 CTGCAAGTGACTATGAGAGGCTTCTACGAGGGCTTTCAAACGCAACCGTGTGGCCTCTTT 2580

Qy  2581 TCCACGATTTGATTGTTACTCCGGTGTACACACCGATTGGTGGCATGGCGTTTCGGGAAG 2640
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Db  2581 TCCACGATTTGATTGTTACTCCGGTGTACACACCGATTGGTGGCATGGCGTTTCGGGAAG 2640

Qy  2641 TAAACCTTCAAGTTCGCTGAAGCGTGAGCGGCCACAGCGTGCCACTGTGTGGG 2700
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Db  2641 TAAACCTTCAAGTTCGCTGAAGCGTGAGCGGCCACAGCGTGCCACTGTGTGGG 2700

Qy  2701 TGCAGGACTATCAGCTGTTGCTGGTTCTCGGCATTTGCGCCAGATGCGCCCTGATTTGA 2760
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Db  2701 TGCAGGACTATCAGCTGTTGCTGGTTCTCGGCATTTGCGCCAGATGCGCCCTGATTTGA 2760

Qy  2761 AGATCCGTTTCTTCCTCCACATTCCCTTCCCTTGTCGTCAGCTGC 2817
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Db  2761 AGATCCGTTTCTTCCTCCACATTCCCTTCCCTTGTCGTCAGCTGC 2817
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RESULT 6
US-10-224-574-9
; Sequence 9, Application US/10224574
; Publication No. US20040101837A1
; GENERAL INFORMATION:
; APPLICANT: Forschungszentrum Jlich GmbH; P. Ziegler, L. Eggeling, H. Sahm,
; APPLICANT: P. Peters- Wendisch
; TITLE OF INVENTION: Nukleotide sequences coding for proteins parcipitating in the syn
; TITLE OF INVENTION: L-Serin, improved process for the microbial manufacture of L-ser
; TITLE OF INVENTION: genetically modified microorganism suitable for the process.
; FILE REFERENCE: PZJ-9912-PCT
; CURRENT APPLICATION NUMBER: US/10/224,574
; CURRENT FILING DATE: 2002-08-21
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
;
; SEQ ID NO 9
; LENGTH: 2817
; TYPE: DNA
; ORGANISM: C. glutamicum ATCC 14 752
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (398)..(1867)

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Db   961  TGCCACGAGCTCATTTTGGGAAAGAAGGGTTGCCTACTTTCTTCCAAAATGTGTTGTGG 1020
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Qy  1021  TGGTTTTATTGCCACGCTGCCTGCCTGCCATCGATCGATTGCTTATTCTTTGGCGTTGCAATTTGGTCT 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1021  TGGTTTTATTGCCACGCTGCCTGCCTGCCATCGATCGATTGCTTATTCTTTGGCGTTGCAATTTGGTCT 1080

Qy  1081  TGAGATCAAACCGAGCCAGATCATCGCATCTCGGAATTGTGTGCGTGTTGGCAGGTTTGAC 1140
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Db  1081  TGAGATCAAACCGAGCCAGATCATCGCATCTCGGAATTGTGTGCGTGTTGGCAGGTTTGAC 1140

Qy  1141  ACTTGTGCAATCTCTGCAGGACGGCATCACGGGCGCTCCGGTGACAGCAAGTGCACGATT 1200
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Db  1141  ACTTGTGCAATCTCTGCAGGACGGCATCACGGGCGCTCCGGTGACAGCAAGTGCACGATT 1200

Qy  1201  TTTTGAAACACTCCTGTTACCGGCCATTGTTGCTGGCTGGGTTTGGGCATTCAGCT 1260
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Db  1201  TTTTGAAACACTCCTGTTACCGGCCATTGTTGCTGGCTGGGTTTGGGCATTCAGCT 1260

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Db  1261  TTCTGAAATCTTGCATGTCATGTTGCCTGCCATGGAGTTCGCTGCAGCACCTAATTATTC 1320

Qy  1321  GTCTACATTCGCCCGCCATTATCGCTGGTGGCGTCACCGCAGCGGCCTTCGCAGTGGGTTG 1380
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Db  1321  GTCTACATTCGCCCGCCATTATCGCTGGTGGCGTCACCGCAGCGGCCTTCGCAGTGGGTTG 1380

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Db  1381  TTACGCGGAGTGGTCCTCGGTGATTATTGCGGGGCTTACTGGCGTTCTGCGTT 1440

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Db  1441  TTATTACCTTCTTCGTTGTTTATTTAGGCCCCGTCTCTCTGCGCGCTGCCTGCCAACAGC 1500

Qy  1501  AGTTGGTTTCACTGGTGTTTGCTTGCCCGTCGATTCCACCGTTGATTGTGGC 1560
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Db  1501  AGTTGGTTTCACTGGTGTTTGCTTGCCCGTCGATTCCACCGTTGATTGTGGC 1560

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Db  1561  GATTGCCGGCATCACACCCAAATGCTTCCAGGTTCCAGGTTCCAGCAATTTACCGCGGAATGTACGGCCAC 1620

Qy  1621  CTTGAATGATCAAACACTCATGGGTTTCACCAACACATTGCGGTTGCTTGCTTTAGCCACTGCTTC 1680
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Db  1621  CTTGAATGATCAAACACTCATGGGTTTCACCAACACATTGCGGTTGCTTGCTTTAGCCACTGCTTC 1680

Qy  1681  ATCACTTGCCGCGGCTGGGCGTGGTTTTGGGTGAGTGAGGATGCCCGCAGGCTACGTCGTCCACC 1740
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Db  1681  ATCACTTGCCGCGGCTGGGCGTGGTTTTGGGTGAGTGAGGATGCCCGCAGGCTACGTCGTCCACC 1740

Qy  1741  ACGCTTCAACCCATACCCATACCGTGCATTTACCAAGGCGAATGAGTTCTCCTTCCAGGAGGAAGC 1800
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Db  1741  ACGCTTCAACCCATACCCATACCGTGCATTTACCAAGGCGAATGAGTTCTCCTTCCAGGAGGAAGC 1800

Qy  1801  TGAGCAGAATCAGCGCCGGCCGCGGCAGAGAAAACGTCCAAAGACTAATCAAAGATTCGGTAATAA 1860
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Db  1801  TGAGCAGAATCAGCGCCGGCCGCGGCAGAGAAAACGTCCAAAGACTAATCAAAGATTCGGTAATAA 1860

Qy  1861  AAGGTAAAAATCAACCTGCTTAGGCGTCTTTCGCTTAAATAGCGTAGAATATCGGGTCGA 1920
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Db  1861  AAGGTAAAAATCAACCTGCTTAGGCGTCTTTCGCTTAAATAGCGTAGAATATCGGGTCGA 1920

Qy  1921  TCGCTTTAAACACTCAGGAGGAGGATCCTTGGCGGATTGAGTGATTCACGGACACTCGTCCCCACC 1980
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1921  TCGCTTTAAACACTCAGGAGGAGGATCCTTGGCGGATTGAGTGATTCACGGACACTCGTCCCCACC 1980

Qy  1981  CAGAATCCCTTCAGCGTTGTTGAAGAGGAAACCGCAGCCGCGTGCCCGCAGGATTGTTGCCA 2040
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1981  CAGAATCCCTTCAGCGTTGTTGAAGAGGAAACCGCAGCCGCGTGCCCGCAGGATTGTTGCCA 2040

Qy  2041  CCTATTCTAAGGACTTCTTCGACGGCGTCACTTTGATGTGCATGCGTCGGCGTTGAACCTC 2100
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Db  2041  CCTATTCTAAGGACTTCTTCGACGGCGTCACTTTGATGTGCATGCGTCGGCGTTGAACCTC 2100
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Qy  2101  AGGGCCTGCGTTACACCAAGGTCGCTTCTGAACACGAGGAAGCTCAGCAGAAGAGGCTA 2160
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Db  2101  AGGGCCTGCGTTACACCAAGGTCGCTTCTGAACACGAGGAAGCTCAGCAGAAGAGGCTA 2160

Qy  2161  CAAAGCCGGACTCGTAAGGCACCAGCTGCTGCTGCTAAGAACGACCAAGAGA 2220
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Db  2161  CAAAGCCGGACTCGTAAGGCACCAGCTGCTGCTGCTAAGAACGACCAAGAGA 2220

Qy  2221  CCACTAAGAAAACTACTAAAAGACACCGCAAAGAGACACCAAAGAAGTCTTAAGCCG 2280
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Db  2221  CCACTAAGAAAACTACTAAAAGACACCGCAAAGAGACACCAAAGAAGTCTTAAGCCG 2280

Qy  2281  GATCTTATATGGATGATTCCAATAGCTTTGTAGTTGTTGCTAACCGTCTGCCAGTGGATA 2340
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Db  2281  GATCTTATATGGATGATTCCAATAGCTTTGTAGTTGTTGCTAACCGTCTGCCAGTGGATA 2340

Qy  2341  TGACTGTCCACCCAGATGGTAGTATAGCATCTCCCCAGCCCGGGTTGGCCTTGTCACGG 2400
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Db  2341  TGACTGTCCACCCAGATGGTAGTATAGCATCTCCCCAGCCCGGGTTGGCCTTGTCACGG 2400

Qy  2401  GGCTTTCCCCGTTCTGGAACACATCGTGATGTTGGGTCGGATGGCCTGGATGGCCTGAACTGTAG 2460
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Db  2401  GGCTTTCCCCGTTCTGGAACACATCGTGATGTTGGGTCGGATGGCCTGGATGGCCTGAACTGTAG 2460

Qy  2461  ATGTTGCACCCGAACCATTCGAACAGATACGGGTGTTTGCTGCACCCGTGTTTGTCCTCA 2520
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Db  2461  ATGTTGCACCCGAACCATTCGAACAGATACGGGTGTTTGCTGCACCCGTGTTTGTCCTCA 2520

Qy  2521  CTGCAAGTGACTATGAAGGCTTCTACGAGGGCTTTCAAACGCAACGCGTGTGGCCCTCTTT 2580
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Db  2521  CTGCAAGTGACTATGAAGGCTTCTACGAGGGCTTTCAAACGCAACGCGTGTGGCCCTCTTT 2580

Qy  2581  TCCACGATTGATTGTTACTCCGGTGTACAACACCGATTGGTGCATGGGGAAG 2640
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Db  2581  TCCACGATTGATTGTTACTCCGGTGTACAACACCGATTGGTGCATGGGGAAG 2640

Qy  2641  TAAACCTCAAGTTCGCTGAAGCCGTGAGCGCCGTGAGCGTGGCGGCACGTGTCGTGTGGG 2700
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Db  2641  TAAACCTCAAGTTCGCTGAAGCCGTGAGCGCCGTGAGCGTGGCGGCACGTGTCGTGTGGG 2700

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Db  2701  TGCAGGACTATCAGCTGTTGCTGGTTCCTGGCATTTTGCGCCAGATGGCGCCGATTTGA 2760

Qy  2761  AGATCCGTTTCTTCCTCCACATTCCCTTCCCTCCCCACATTCCGTCTGTTCCGTCAGCTGC 2817
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; PRIOR APPLICATION NUMBER: JP 00/280988
; PRIOR FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 7059
; SOFTWARE: PatentIn ver. 3.0
; SEQ ID NO 1
; LENGTH: 3309400
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
US-09-738-626-1

Query Match          98.8%;  Score 2783.4;  DB 9;  Length 3309400;
Best Local Similarity 99.3%;  Pred. No. 0;
Matches 2796;  Conservative 0;  Mismatches 21;  Indels 0;  Gaps 0;

Qy        1 AATGAAATAATCCCTCACCAACTGGGCAATCAAACACCGTTCAATTCCAAACATCG 60
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Db  2790585 AATGAAATAATCCCTCACCAACTGGGCAGATCAAACACCGTTCAATTCCAAACATCG 2790644

Qy       61 AGCCAAGGGAAAAGAAAGCCCCTAAGCCCGTGTTATTAAAATGGAGACTCTTTGGAGACC 120
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Qy      121 TCAAGCCAAAAGGGGCATTTTCATTAAGAAAATACCCCTTTGACCTGGTGTTATTGAGC 180
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Db  2790705 TCAAGCCAAAAGGGGCATTTTCATTAAGAAAATACCCCTTTGACCTGGTGTTATTGAGC 2790764

Qy      181 TGGAGAGAGACTGAACTCTCAACCTACGCATTACAAGTGCGTGCGCTGCCAATTGCG 240
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Qy      241 CCACTCCAGCACCCGACAGTGCTGATGATCAACAACTACGAATCTATCTTAGCGTATGT 300
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Db  2790825 CCACTCCAGCACCCGACAGTGCTGATGATCAACAACTACGAATCTATCTTAGCGTATGT 2790884

Qy      301 GTACATCACAATGGAATTCGGGCTACTAGATATCGGGTGAACCTGCATAAACGACCTGTG 360
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Db  2790885 GTACATCACAATGGAATTCGGGCTACTAGATATCGGGTGAACCTGCATAAACGACCTGTG 2790944

Qy      361 ATTGGACTCTTTTTCCTTGCAAAATGTTTCCAGCGGATGTGAGTTTGCGACCCCTTCG 420
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Db  2790945 ATTGGACTCTTTTTCCTTGCAAAATGTTTCCAGCGGATGTGAGTTTGCGACCCCTTCG 2791004

Qy      421 TGGCCGCATTTCAACAGTTGACGCTGCAAAAGCCGCACCTCCGCCACTAGCCCC 480
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Db  2791005 TGGCCGCATTTCAACAGTTGACGCTGCAAAAGCCGCACCTCCGCCACTAGCCCC 2791064

Qy      481 GATTGATCTCACTGACCATAGTCAAGTGCCGGTGTGATGAATTGGCTGCGAGAATTGG 540
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Qy      541 CGATATTTGCTTTCTTCCTTGCTTCTTCAGGTGACGTCAAACAGTGATCAAGGTGCAAGTTCGAGGCGGT 600
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Db  2791125 CGATATTTTGCTTTCTTCCTTGCTTCTTCAGGTGACGTCAAATAGTGACAACCAAGGTACAAGTTCGAGGCAGT 2791184

Qy      601 GACCTCTGCGTATGGCCTGTACTATACACGCATGTGGATATCACGTTGAATACGATCACCAT 660
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Db  2791185 GACCTCTGCGTATGGCCTGTACTATACACGCATGTGGATATCACGTTGAATACGATCACCAT 2791244

Qy      661 CTTCACCAACATCGGTGTGGAGAGGAAGATGCCGGTCAACGTGTTTCATGTTGTGGGCAA 720
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Db  2791245 CTTCACCAACATCGGTGTGGAGAGGAAGATGCCGGTCAACGTGTTTCATGTTGTGTAGGCAA 2791304

Qy      721 GTTGGGACACCAACTTCTCCAAACTGTCTGAGGTTGACCGGTTGATCCGTTCCATTCAGGC 780
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Db  2791305 GTTGGGACACCAACTTCTCCAAACTGTCTGAGGTTGACCGGTTGATCCGTTCCATTCAGGC 2791364

Qy      781 TGGTGCTACCCCCGCCTGAGGTTGCCGAGTTGGAGCAATCGCCTGC 840
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Db  2791365 TGGTGCGACCCCCGCCTGAGGTTGCCGAGTTGGAGCAATCGCCTGC 2791424

Qy      841 GTCTTATGGTTTCCCTGTTGCGTGGCGTTGCGTTGCGTTGGGCAATGATGGGTGCGTGTTGCTGT 900
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Db  2791425 GTCTTTATGGTTTCCCTGTTGCGTGGCGTTGCGTTGCGTTGGGCAATGATGGGTGCGTGTTGCTGT 2791484

Qy      901 GCTGTTGGGTGGGTGGATGGCAGGTTCCCTAATTGCTTTATTACCGCGTTCACGATCAT 960
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Db  2791485 GCTGTTGGGTGGGTGGATGGCAGGTTCCCTAATTGCTTTATTACCGCGTTCACGATCAT 2791544

Qy      961 TGCCACGACGTCATTTTGGGAAAGAAAGGTTTGCCTACTTCTTCCAAAATGTGTTGG 1020
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Db  2791545 TGCCACGACGTCATTTTGGGAAAGAAAGGTTTGCCTACTTCTTCCAAAATGTGTTGG 2791604

Qy     1021 TGGTTTTATTGCACGCTGCCTGCATCGATTGCTTATTCTTTGGCGTTGCAATTGGTCT 1080
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Db  2791605 TGGTTTTATTGCCACGCTGCCTGCATCGATTGCTTATTCTTTGGCGTTGCAATTGGTCT 2791664

Qy     1081 TGAGATCAAACCGAGCCAGATCATCGCATCTGGAATTGTTGTGCTGTTGGCAGGTTTGAC 1140
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Db  2791665 TGAGATCAAACCGAGCCAGATCATCGCATCTGGAATTGTTGTGCTGTTGGCAGGTTTGAC 2791724

Qy     1141 ACTTGTGCAATCTCTGCAGGACGGCATCACAGGGGCTCCGGTGACAGCAAGTGCACGATT 1200
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Db  2791725 ACTCGTGCAATCTCTGCAGGACGGCATCACAGGGGCTCCGGTGACAGCAAGTGCACGATT 2791784

Qy     1201 TTTTGAAACACTCCGTGTTACCGGCGGCATTGTTGCTCGGCGGTGGGCATTCAGCT 1260
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Db  2791785 TTTCGAAACACTCCGTGTTACCGGCGGCATTGTTGCTCGGCGGTGGGCATTCAGCT 2791844

Qy     1261 TCCTGAAATCTTGCATGTCATGTCCGCTGCCATGGAGTCCGCTGCGAGCACCTAATTATTC 1320
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Db  2791845 TTCTGAAATCTTGCATGTCATGTCCGCTGCCAATGGAGTCCGCTGCGAGCACCTAATTATTC 2791904

Qy     1321 GTCTACAATCGCCCGCATTATCGCTGGTGGCGTCACCGGCCTTCGCAGCGGCCTTCGCAGTATGT 1380
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Db  2791905 GTTCTACAATTCGCCCGCATTATCGCTGGTGGCGTCACCGGCCTTCGCAGCGGCCTTCGCAGTATGT 2791964

Qy     1381 TTACGCGGAGTGGTCCTCCGGTGATTATTGCGGGGCTTACTGCGTTCACCGGCTTGCGTT 1440
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Db  2791965 TTACGCGGAGTGGTCCTCCGGTGATTATTGCGGGGCTTACTGCGTTCACCGGCTTGCGTT 2792024

Qy     1441 TTATTACCTTCTTCGTGTTGTTATTTAGGCCCGTCTCTGCGCGTCTGCGATTGCTGCAACAGC 1500
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Db  2792025 TTATTACCTTCTTCGTGTTGTTATTTAGGCCCGTCTCTGCGCGTCTGCGATTGCTGCAACAGC 2792084

Qy     1501 AGTTGGTTTCACTGGTGGTTGCTTGCCCGTCGATTCTTGATTGCGGC 1560
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Db  2792085 AGTTGGTTTCACTGGTGGTTGCTTGCCCGTCGATTCTTGATTGCGGC 2792144

Qy     1561 GATTGCCGGCATCACACCAATGCTTCCAGGTCAGTTTAGCCAATTTACCGCGGGAATGTACGCCAC 1620
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Db  2792145 GATTGCCGGCATCACACCAATGCTTCCAGGTCAGTTTAGCCAATTTACCGCGGGAATGTACGCCAC 2792204

Qy     1621 CTTGAATGATCAAACACTCATGGGTTTGCTTTAGCCACTGCTTC 1680
            ||||||||||||||||||||||||||||||||||||||||||||
Db  2792205 CCTGAATGATCAAACACTCATGGGTTTGCTTTAGCCACTGCTTC 2792264

Qy     1681 ATCACTTGCCGCGTTGGCGTGGTTTTGGGTGAGTGGATTGCCGCAGGCTACGTCGTTCCACC 1740
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2792265 ATCACTTGCCGCGTTGGCGTGGTTTTGGGTGAGTGGATTGCCGCAGGCTACGTCGTTCCACC 2792324

Qy     1741 ACGCTTCAACCATACCGTGCATTTACCAAGGCGAATGAGTTCTCCTTCCAGAGGAAGC 1800
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Db  2792325 ACGCTTCAACCATACCGTGCATTTACCAAGGCGAATGAGTTCTCCTTCCAGAGGAAGC 2792384

Qy     1801 TGAGCAGAATCAGCGCCGGCAGAGAAAACGTCAAAGATTCGGTAATAA 1860
            |||||||||||||||||||||||||||||||||||||||||||||||||
Db  2792385 TGAGCAGAATCAGCGCCGGCAGAGAAAACGTCAAAGATTCAGAGATTCGGTAATAA 2792444

Qy     1861 AAGTAAAAATCAACCTGCTTAGGCGTCTTCGCTTAAATAGCGTAGAATATCGGGTCGA 1920
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2792445 AAGTAAAAATCAACCTGCTTAGGCGTCTTTCGCTTAAATAGCGTAGAATATCGGGTCGA 2792504

Qy     1921 TCGCTTTTAAACACTCAGGAGGATCCTTGCGGCCAAAATCACGGACACTCCGTCCCACCC 1980
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Db  2792505 TCGCTTTTAAACACTCAGGAGGATCCTTGCGGCCAAAATCACGGACACTCCGTCCCACCC 2792564
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Qy   1981  CAGAATCCTTCACGCTGTTGAGAGAGAAACCGCAGCCGGTGCCCGAGGATTGTTGCCA  2040
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Db 2792565  CAGAATCCTTCACGCTGTTGAGAGAGAAACCGCAGCCGGTGCCCGAGGATTGTTGCCA  2792624

Qy   2041  CCTATTCTAAGGACTTCTTCGACGGCGTCACTTGATGTGCATGCTCGGCGTTGAACCTC  2100
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2792625  CCTATTCTAAGGACTTCTTCGACGGCGTCACTTGATGTGCATGCTCGGCGTTGAACCTC  2792684

Qy   2101  AGGGCCTGCGTTACACCAAGTCGCTTCTGAACACGAGGAAGCTCAGCCAAAGAAGCTA  2160
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Db 2792685  AGGGCCTGCGTTACACCAAGTCGCTTCTGAACACGAGGAAGCTCAGCCAAAGAAGCTA  2792744

Qy   2161  CAAAGCCGACTCGTAAGGCACCAGCTAAGAACGCTGCTCTAAGAAAACGACCAAGAGA  2220
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Db 2792745  CAAAGCCGACTCGTAAGGCACCAGCTAAGAACGCTGCTCTAAGAAAACGACCAAGAGA  2792804

Qy   2221  CCACTAAGAAAACTACTAAAAAGACCACCCGCAAAGAAGAAGCACCAAAGAAGTCTTAAGCCG  2280
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Db 2792805  CCACTAAGAAAACTACTAAAAAGACCACCCGCAAAGAAGAAGCACCAAAGAAGTCTTAAGCCG  2792864

Qy   2281  GATCTTATATGGATGATTCCAATAGCTTTGTAGTTGTTGCTAACCGTCTGCGCAGTCGGATA  2340
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Db 2792865  GATCTTATATGGATGATTCCAATAGCTTTGTAGTTGTTGCTAACCGTCTGCGCAGTCGGATA  2792924

Qy   2341  TGACTGTCCACCCAGATGGTAGCTATAGCATCTCCCCCAGCCCCGTGGCCTTGTCACGG  2400
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Db 2792925  TGACTGTCCACCCAGATGGTAGCTATAGCATCTCCCCCAGCCCCGTGGCCTTGTCACGG  2792984

Qy   2401  GGCTTTCCCCCGTTCTGGAACAACATCGTGGATGTTGGGTCGGATGGCCTGGAACTGTAG  2460
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2792985  GGCTTTCCCCCGTTCTGGAACAACATCGTGGATGTTGGGTCGGATGGCCTGGAACTGTAG  2793044

Qy   2461  ATGTTGCACCCGAACCATTCGAACAGATACGGGTGTTTCGCTCGTGCACCCTGTGTCCTCA  2520
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Db 2793045  ATGTTGCACCCGAACCATTCGAACAGATACGGGTGTTTCGCTCGTGCACCCTGTGTCCTCA  2793104

Qy   2521  CTGCAAGTGACTATGAAGGCTTCACGAGGCTTTCAAACGCAACGCTGTGCCTCTTT  2580
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Db 2793105  CTGCAAGTGACTATGAAGGCTTCACGAGGCTTTCAAACGCAACGCTGTGCCTCTTT  2793164

Qy   2581  TCCACGATTTGATTGTTACTCCGGTGTACACACCGATTGTGGCATGCGTTTCGGGAAG  2640
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2793165  TCCACGATCTGATTGTTACTCCGGTGTACACACCGATTGTGGCATGCGTTTCGGGAGG  2793224

Qy   2641  TAAACCTTCAAGTTCGCTGAAGCCGTGAGCCAAGTGGCGCACACGTGCCACTGTGTGGG  2700
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2793225  TAAACCTTCAAGTTCGCTGAAGCCGTGAGCCAAGTGGCGCACACGTGCCACTGTGTGGG  2793284

Qy   2701  TGCAGGACTATCAGCTGTTGCTGGTTCCTGGCATTTGCGCCAGATGCGCCCTGATTTGA  2760
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2793285  TGCAGGACTATCAGCTGTTGCTGGTTCCTGGCATTTGCGCCAGATGCGCCCTGATTTGA  2793344

Qy   2761  AGATCCGGTTTCTTCCTCCACATTCCCTTCCCTTCCCTTCCCCGATCTGTTCCGTCAGCTGC  2817
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2793345  AGATCCGGTTTCTTCCTCCACATTCCCTTCCCTTCCCCGATCTGTTCCGTCAGCTGC  2793401
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;   PRIOR FILING DATE: 1999-11-01
;   NUMBER OF SEQ ID NOS: 10
;   SOFTWARE: PatentIn Ver. 2.1
;   SEQ ID NO 3
;   LENGTH: 1909
;   TYPE: DNA
;   ORGANISM: Corynebacterium glutamicum
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (280)..(1746)
;   OTHER INFORMATION: thrB-Gen
US-09-951-536-3

Query Match       65.2%;    Score 1836.6;    DB 9;    Length 1909;
Best Local Similarity 99.0%;  Pred. No. 0;
Matches 1848;  Mismatches 19;  Conservative 0;  Indels 0;  Gaps 0;
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Qy   156  CCCCTTTGACCTGGTGTTATTGAGCTGGAGGAGAGACTTGAACTCTCAACCTACGCATTA  215
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Db    38  CCCCTTTGACCTGGTGTTATTGAGCTGGAGGAGAGACTTGAACTCTCAACCTACGCATTA  97

Qy   216  CAAGTGCGTTGCGCTGCCAATTGCGCCACTCCAGCACCGCAGATGCTGATGATCAACAAC  275
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Db    98  CAAGTGCGTTGCGCTGCCAATTGCGCCACTCCAGCACCGCAGATGCTGATGATCAACAAC  157

Qy   276  TACGAATACGTATCTTAGCGTATGTGTACATCACAATGGAATTCGGGGCTAGAGTATCTG  335
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Db   158  TACGAATACGTATCTTAGCGTATGTGTACATCACAATGGAATTCGGGGCTAGAGTATCTG  217

Qy   336  GTGAACCGTGCATAAACGACCTGTGATTGAGCTCTTTTCCTTGCAAAATGTTTTCCAGC  395
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Db   218  GTGAACCGTGCATAAACGACCTGTGATTGAGCTCTTTTCCTTGCAAAATGTTTTCCAGC  277

Qy   396  GGATGTTGAGTTTGCGACCCTTCGTGCCGCCCATTCAACAGTTGACGTCGCAAAAGCCG  455
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   278  GGATGTTGAGTTTGCGACCCTTCGTGCCGCCCATTCAACAGTTGACGTCGCAAAAGCCG  337

Qy   456  CACCTCCGCCATCGCCACTAGCCCCGATTGATCTCACTGACCATAGTCAAGTGGCCGGTG  515
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   338  CACCTCCGCCATCGCCACTAGCCCCGATTGATCTCACTGACCATAGTCAAGTGGCCGGTG  397

Qy   516  TGATGAATTGGCTGCGAGAATTGGCGCATATTTGCTTCTTCAGGTACGTACGTCAAACAGTG  575
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Db   398  TGATGAATTGGCTGCGAGAATTGGCGCATATTTGCTTCTTCAGGTACGTACGTCAAATAGTG  457

Qy   576  ATACCAAGGTGCAAGTTCGAGCGGTGACCTCGCGTATGGCCTGTATACGACCCATGTGG  635
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Db   458  ACACCAAGGTACAAGTTCGAGCAGTTGACCTCGCGTATGGTTTGTACTACGACGACGTGG  517

Qy   636  ATATCACGTTGAATACGATCACCATCTTCACCAACATCGGTGTGGAGAGGAAGATGCCGG  695
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Db   518  ATATCACGTTGAATACGATCACCATCTTCACCAACATCGGTGTGGAGAGGAAGATGCCGG  577

Qy   696  TCAACGTTGTTTCATGTTGTGGGGCAAGTTGGACACCAACTTCTCCAAACTTCTGGAGGTTG  755
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   578  TCAACGTTGTTTCATGTTGTGGGGCAAGTTGGACACCAACTTCTCCAAACTTCTGGAGGTTG  637

Qy   756  ACCGTTTGATCCGTTCCATTCAGGCTGGTGCTACCCCGGCCTCACCCCGAGGTTGCCGAGAAAATTC  815
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Db   638  ACCGTTTGATCCGTTCCATTCAGGCTGGTGCTACCCCGGCCTCACCCCGAGGTTGCCGAGAAAATCC  697

Qy   816  TGGACGAGTTGGAGCAATCGCCTCGCGTCTTATGGTTTCCCGTTGCTTGGCTGGG  875
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Db   698  TGGACGAGTTGGAGCAATCCCCGTCGCGTCTTATCGTTTCCCGTTGCTTGGCTGGG  757

Qy   876  CAATGATGGGTGGCGCTGTTGCTGTGTCGTTGGGTGGCAGGTTCCCTAATTG  935
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   758  CAATGATGGGTGGCGCTGTTGCTGTGTCGTTGGGTGGCAGGTTCCCTAATTG  817

Qy   936  CTTTTATTACCGCGTTCACGATCATTGCCACGATCATTTTTGGAAAGAAGGGTTTGC  995
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Db   818  CTTTTATTACCGCGTTCACGATCATTGCCACGATCATTTTTGGAAAGAAGGGTTTGC  877
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RESULT 8
US-09-951-536-3
; Sequence 3, Application US/09951536
; Patent No. US2002010737SA1
; GENERAL INFORMATION:
;   APPLICANT: ZIEGLER, PETRA
;   APPLICANT: EGGELING, LOTHAR
;   APPLICANT: SAHM, HERMANN
;   APPLICANT: THIERBACH, GEORG
;   TITLE OF INVENTION: NEW NUCLEOTIDE SEQUENCES CODING FOR THE THRE GENE AND
;   TITLE OF INVENTION: PROCESS FOR THE ENZYMATIC PRODUCTION OF L-THREONINE
;   TITLE OF INVENTION: USING CORYNEFORM BACTERIA
;   FILE REFERENCE: 21123/282414/MAS
;   CURRENT APPLICATION NUMBER: US/09/951,536
;   CURRENT FILING DATE: 2001-09-14
;   PRIOR APPLICATION NUMBER: 09/431,099
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RESULT 9
US-09-963-521-3
; Sequence 3, Application US/09963521
; Patent No. US2002014678lA1
; GENERAL INFORMATION:
; APPLICANT: ZIEGLER, PETRA
; APPLICANT: EGGELING, LOTHAR
; APPLICANT: SAHM, HERMANN
; TITLE OF INVENTION: NEW NUCLEOTIDE SEQUENCES CODING FOR THE THRE GENE
; TITLE OF INVENTION: AND PROCESS FOR THE ENZYMATIC PRODUCTION OF
; TITLE OF INVENTION: L-THREONINE USING CORYNEFORM BACTERIA
; FILE REFERENCE: 21123/282413/MAS
; CURRENT APPLICATION NUMBER: US/09/963,521
; CURRENT FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: 09/431,099
; PRIOR FILING DATE: 1999-11-01
; PRIOR APPLICATION NUMBER: DE 199 41 478.5
; PRIOR FILING DATE: 1999-09-01
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 1909
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (280)..(1746)
; OTHER INFORMATION: thrB-Gen
US-09-963-521-3

Query Match   65.2%;   Score 1836.6;   DB 9;   Length 1909;
Best Local Similarity 99.0%;   Pred. No. 0;
Matches 1848;   Conservative 0;   Mismatches 19;   Indels 0;   Gaps 0;

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Qy    156 CCCCTTTGACCTGGTGTTATTGAGCTGGAAGAGACTGAACTCTCAACCTACGCATTA 215
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     38 CCCCTTTGACCTGGTGTTATTGAGCTGGAAGAGACTGAACTCTCAACCTACGCATTA 97

Qy    216 CAAGTGCGTTGCGCTGCCAATTGCCCAGTGCTGATGATCAACAAC 275
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Db     98 CAAGTGCGTTGCGCTGCCAATTGCCCAGTGCTGATGATCAACAAC 157

Qy    276 TACGAATACGTATCTTAGCGTATGTGTACATCACAATGCATCACAATGCTAGAGTGTATCTG 335
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy    336 GTGAACCGTGCATAAACGACCTGTGATTGGACTCTTTTTCCTTGCAAAATGTTTTCCAGC 395
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Qy    396 GGATGTGTGAGTTTTGGCGACCCTTCGTGGCGCCATTCAACAGTTGACGCGTCGAAAGCCG 455
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Qy    516 TGATGAATTGGCTGCGAGAATTGGCGAGCGGTGACCTCGGTCAAACAGTG 575
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Db    398 TGATGAATTGGCTGCGAGAATTGGCGAGCGGTGACCTCGGTCAAACAGTG 457

Qy    576 ATACCAAGGTGCAAGTTCGAGCGGTGACCTGCCTTGTACTACTACAGCGATGTGG 635
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Db    458 ACACCAAGGTACAAGTTCGAGCGGTGACCTGCCTTGTACTACTACAGCGATGTGG 517

Qy    636 ATATCACGTTGAATACGATCACCATCTTCACCACATCCGGTGTGGAGAGGAAGATGCCGG 695
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Db    578 TCAACGTGTTTCATGTTGTAGGCAAGTTGGACACCAACTTCTCCAAACTGTCTGAGGTTG 637
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Qy    996 CTACTTTCTTCCAAAATGTGTTGGTGGTTTATTGCCACGCTGCCTGCATCGATTGCTT 1055
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Db    938 ATTCTTTGGCGTTGCAATTGGTCTTGAGATCAAACCGAGCCAGATCATCGCATCGGAA 997

Qy   1116 TTGTTGTGCTGTTGGCAGGTTTGACACTTGTCAATCTCTGCGAGGACGGCATCACGGGCG 1175
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    998 TTGTTGTGCTGTTGGCAGGTTTGACACTTGTCAATCTCTGCGAGGACGGCATCACGGGCG 1057

Qy   1176 CTCCGGTGACAGCAAGTGCACGATTTTTGAAACACTCCTGTTTACCGGCGGCATTGTTG 1235
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Db   1118 CTGGCGTGGGTTTGGGCATTCAGCTTTCTGAAAATCTTGCATGTCATGTTGCCTGCCATGG 1177

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Db   1178 AGTCCGCTGCAGCACCTAATTATTCGTCTACATTCGCCCGCGCATTATCGCTGTGTGGGCGTCA 1237

Qy   1356 CCGCAGCGGCCTTCGCAGTGGGTGTTACGCGAGTGGTCCTCGGTCGATTATTGCGGGGC 1415
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Db   1598 TTGCCCGCAGGCTACGTCGTCGTCCACCACGCTTCAACCGCTTCAACCTGCATTACCAAGGCGA 1657

Qy   1776 ATGAGTTCTCCTTCCAGGAGAAGCTGAGCAGAATCAGCGCCGGCGGAGAAAACGTCCAA 1835
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Db   1658 ATGAGTTCTCCTTCCAGGAGAAGCTGAGCAGAATCAGCGCCGGCGGAGAAAACGTCCAA 1717

Qy   1836 AGACTAATCAAAGATTCGGTGTAATAAAGTAAAATCAACCTGCTTAGGCGCTCTTTCGCT 1895
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Db   1718 AGACTAATCAGAGATTCGGTGTAATAAAGTAAAATCAACCTGCTTAGGCGCTCTTTCGCT 1777

Qy   1896 TAAATACGGTAGAATATCGGGTCGATCGCTTTAAACACTCAGGAGGATCCTTGCCCGCC 1955
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1778 TAAATAGCGTAGAATATCGGGTCGATCGCTTTAAACACTCAGGAGGATCCTTGCCCGCC 1837

Qy   1956 AAAATCACGGACACTCGTCCCACCCCAGAAATCCCTTGTTGAAGAGGAAAACCGCA 2015
          |||||||||| |||||||||||||||||||||||||||||||||||||||||||||
Db   1838 AAAATCACGGACACTCGTCCCACCCCCAGAAATCCCTTGTTGAAGAGGAAAACCGCA 1897

Qy   2016 GCCGGGTG 2022
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Db   1898 GCCGGGG 1904
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Qy 1836 AGACTAATCAAAGATTCGTAATAAATAAAAGTAATAAAATCAACCTGCTTAGGCGTCTTCGCT 1895
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Db 1718 AGACTAATCAGAGATTCGTAATAAATAAAAGTAATAAAATCAACCTGCTTAGGCGTCTTCGCT 1777

Qy 1896 TAAATAGCGTAGAATATCGGGTCGATCGCTTTTAAACACTCAGGAGGATCCTTGCCGGCC 1955
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Db 1778 TAAATAGCGTAGAATATCGGGTCGATCGCTTTTAAACACTCAGGAGGATCCTTGCCGGCC 1837

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Qy 2016 GCCGGTG 2022
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Db 1898 GCCGGGG 1904

RESULT 10
US-09-834-721-3
; Sequence 3, Application US/09834721
; Patent No. US2002015551A1
; GENERAL INFORMATION:
; APPLICANT: RIEPING, MECHTHILD
; TITLE OF INVENTION: PROCESS FOR THE FERMENTATIVE PREPARATION OF L-THREONINE
; FILE REFERENCE: 21123/280169/MAS
; CURRENT APPLICATION NUMBER: US/09/834,721
; CURRENT FILING DATE: 2001-04-16
; PRIOR APPLICATION NUMBER: DE 100 26 494.8
; PRIOR FILING DATE: 2000-05-27
; PRIOR APPLICATION NUMBER: DE 101 02 823.7
; PRIOR FILING DATE: 2001-01-23
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 1909
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; FEATURE:
; OTHER INFORMATION: ATCC13032
; NAME/KEY: CDS
; LOCATION: (280)..(1746)
; OTHER INFORMATION: thrE gene
US-09-834-721-3

Query Match   65.2%; Score 1836.6; DB 9; Length 1909;
Best Local Similarity 99.0%; Pred. No. 0;
Matches 1848; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

Qy   156 CCCCTTTGACCTGGTGTTATTGAGCTGGAGAGACTTGAACTCTCAACCTACGCATTA 215
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Db   38 CCCCTTTGACCTGGTGTTATTGAGCTGGAGAGACTTGAACTCTCAACCTACGCATTA 97

Qy   216 CAAGTGCGTTGCGCTGCCAATTGCCCACTCCAGCACCGAGATGCTGATGATCAACAAC 275
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Qy   276 TACGAATACGTATCTTAGCGTATGTACATGTACGGGCTTAGAGTATCTG 335
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Db   158 TACGAATACGTATCTTAGCGTATGTACATGTACGGGCTTAGAGTATCTG 217

Qy   336 GTGAACCGTGCATAAACGACCTGTGATTGGACTCTTTCCTTGCAAAATGTTTTCCAGC 395
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Db   338 CACCTTCCGCCATGCCAGCTAGCCCCTAGCCCCGATTGATCTCACTGACCATAGTCAAGTCAAGTGGCCGGTG 397

Qy   516 TGATGAATTTGGCTGCGGAGAATTGGCGATATTTGCTTTCTTCAGTGACGTCAAACAGTG 575

Qy   756 ACCGTTGATCCGTTCCATTCAGGCTGTGCTACACCCGCCTGAGGTTGCCGAGAAATTC 815
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Qy   816 TGGACGAGTTGGAGCAATCGCCTGCGTCTGCGTTCCCTGTTGCGTTGCTTGGCTGGG 875
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Qy   876 CAATGATGGGTGGCGCTGTTGCTGTGCTGTTGGGTGGTGATGGCAGGTTTCCCTAATTG 935
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Qy   936 CTTTTATTACCGCGTTCACGACGTCATTGCCACGACGTCATTTTTGGGAAAGAAGGGTTTGC 995
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Qy   996 CTACTTTCTCCAAAATGTTGTTGGTGGTGTTTATTGCCACGCTGCCTGCATCGATTGCTT 1055
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Qy 1056 ATTCTTTGGCGTTGCAATTTGGTCTTGAGATCAAACCAGATCAAACCAGATCATCGCGATCATCGCGATCTCGAA 1115
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Db   938 ATTCTTTGGCGTTGCAATTTGGTCTTGAGATCAAACCAGATCAAACCAGATCATCGCGATCATCGCGATCTCGAA 997

Qy 1116 TTGTTGTGCTGTTGGCAGGTTTGACACTTGGACGGGCGCATCACGGGCG 1175
         |||||||||||||||||||||||||||||||||||||||||||||||||
Db   998 TTGTTGTGCTGTTGGCAGGTTTGACACTTGGACGGGCGCATCACGGGCG 1057

Qy 1176 CTCCCGGTGACAGCAAGTGCACGATTTTTGAAACACTTCCTGTTACCGGCGGCCATTGTTG 1235
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1058 CTCCCGGTGACAGCAAGTGCACGATTTTTGAAACACTTCCTGTTACCGGCGGCCATTGTTG 1117

Qy 1236 CTGGCGTGGGTTTGGGCATTCAGCTTTCTGAAAATCTTGCGTCATGTCATGTTGCCTGCCATGG 1295
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1118 CTGGCGTGGGTTTGGGCATTCAGCTTTCTGAAAATCTTGCGTCATGTCATGTTGCCTGCCATGG 1177

Qy 1296 AGTCCGCTGCAGCACCTAATTATTCGTCTACATTCGCCCGCATTATCGCTGGTGGCGTCA 1355
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1178 AGTCCGCTGCAGCACCTAATTATTCGTCTACATTCGCCCGCATTATCGCTGGTGGCGTCA 1237

Qy 1356 CCGCAGGGGCCTTCGCAGTGGGTGTTGTACGCGGAGTGGTCCTCGGGTTATTGCGGGGC 1415
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1238 CCGCAGGGGCCTTCGCAGTGGGTGTTGTACGCGGAGTGGTCCTCGGGTTATTGCGGGGC 1297

Qy 1416 TTACTGCCCTGATGGGTTCTGCGGTTTCGCGTTTGTTGTTATTCTTTAGGCCCCGTCT 1475
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1298 TTACTGCCCTGATGGGTTCTGCGGTTTCGCGTTTGTTGTTATTCTTTAGGCCCCGTCT 1357

Qy 1476 CTGCCCGCTGCGATTGCTGCAACAGCAGTTGGTTTGCTTGCTTGCCCCGTCGAT 1535
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1358 CTGCCCGCTGCGATTGCTGCAACAGCAGTTGGTTTGCTTGCTTGCCCCGTCGAT 1417

Qy 1536 TCTTGATTCCACCGGTTGCTTTAGCCACTCGTTGGCGCATCACACCAATGCTTCCAGGTCTAG 1595
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1418 TCTTGATTCCACCGGTTGCTTTAGCCACTCGTTGGCGCATCACACCAATGCTTCCAGGTCTAG 1477

Qy 1596 CAATTTACCGCCGGAATGTACGCCACCTTGAATGATCAAACTCATGGGTTTCACCAACA 1655
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1478 CAATTTACCGCCGGAATGTACGCCACCTTGAATGATCAAACTCATGGGTTTCACCAACA 1537

Qy 1656 TTGCGGTTGCTTTAGCCAGGCTACGTCGTCCGCTGGCGGTTTTGGGTGAGTGGA 1715
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1538 TTGCGGTTGCTTTAGCCAGGCTACGTCGTCCGCTGGCGGTTTTGGGTGAGTGGA 1597

Qy 1716 TTGCCCGCAGGCTACGGCTTCGTCCACCATACCGTGCATTCAACCGTGCATTCAACAGGGCGA 1775
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1598 TTGCCCGCAGGCTACGGCTTCGTCCACCATACCGTGCATTCAACCGTGCATTCAACAGGGCGA 1657

Qy 1776 ATGAGTTCTCTCCTTCCAGGAGGAAGCTGAGCGCAGAGAGAAACGTCCAA 1835
         |||||||||||||||||||||||||||||||||||||||||||||||||
Db 1658 ATGAGTTCTCTCCTTCCAGGAGGAAGCTGAGCGCAGAGAGAAACGTCCAA 1717

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Db    1478  CAATTACCGCGGAATGTACGCCACCCTGAATGATCAAACACTCATGGGTTTCACCAACA  1537
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    1656  TTGCGGTTGCTTTAGCCACTGCTTCATCACTTGCCCGCTGGCTGGTTGGGTGAGTGGA    1715

Db    1538  TTGCGGTTGCTTTAGCCACTGCTTCATCACTTGCCCGCTGGCTGGTTGGGTGAGTGGA    1597
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    1716  TTGCCCGGAGCTACGTCGTCCACCACGCTTCAACCCATACGTGCATTTACCAAGGCGA    1775

Db    1598  TTGCCCGGAGCTACGTCGTCCACCACGCTTCAACCCATACGTGCATTTACCAAGGCGA    1657
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    1776  ATGAGTTCTCCTTCCAGGAGGAAGCTGAGCAGAATCAGCGCCGGCAGAAACGTCCAA    1835

Db    1658  ATGAGTTCTCCTTCCAGGAGGAAGCTGAGCAGAATCAGCGCCGGCAGAAACGTCCAA    1717
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    1836  AGACTAATCAAAGATTCGGTAATAAAAGTAAAAATCAACCTGCTTAGGCGTCTTCGCT   1895

Db    1718  AGACTAATCAGAGATTCGGTAATAAAAGTAAAAATCAACCTGCTTAGGCGTCTTCGCT   1777
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    1896  TAAATAGGCTAGAATATCGGGTCGATCGTTTAAACACTCAGGAGGATCCTTGCCGGCC   1955

Db    1778  TAAATAGGCTAGAATATCGGGTCGATCGTTTAAACACTCAGGAGGATCCTTGCCGGCC   1837
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Qy    1956  AAAATCACGGACACTCGTCCACCCCAGAATCCCTTCACGCTGTTGAAGAGGAAACCGCA  2015

Db    1838  AAAATCACGGACACTCGTCCACCCCAGAATCCCTTCACGCTGTTGAAGAGGAAACCGCA  1897
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Qy    2016  GCCGGTG  2022

Db    1898  GCCGGGG  1904
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RESULT 11
US-09-783-388-3
; Sequence 3, Application US/09783388
; Patent No. US2002016873A1
; GENERAL INFORMATION:
;   APPLICANT: Ziegler, Petra
;   APPLICANT: Eggeling, Lothar
;   APPLICANT: Sahm, Hermann
;   APPLICANT: Thierbach, Georg
;   TITLE OF INVENTION: NEW NUCLEOTIDE SEQUENCES CODING FOR THE THRE GENE AND
;   TITLE OF INVENTION: PROCESS FOR
;   TITLE OF INVENTION: ENZYMATIC PRODUCTION OF L-THREONINE USING CORYNEFORM BACTERIA
;   FILE REFERENCE: 21123/277066
;   CURRENT APPLICATION NUMBER: US/09/783,388
;   CURRENT FILING DATE: 2001-02-15
;   NUMBER OF SEQ ID NOS: 8
;   SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
;   LENGTH: 1909
;   TYPE: DNA
;   ORGANISM: Corynebacterium glutamicum ATCC13032
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (280)..(1746)
US-09-783-388-3

Query Match   65.2%;   Score 1836.6;   DB 9;   Length 1909;
Best Local Similarity 99.0%;   Pred. No. 0;
Matches 1848;   Conservative 0;   Mismatches 19;   Indels 0;   Gaps 0;

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Qy    156  CCCCTTTGACCTGGTGTTATTGAGCTGAGAAGAGACTTGAACTCTCAACCTACGCATTA   215
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Db     38  CCCCTTTGACCTGGTGTTATTGAGCTGAGAAGAGACTTGAACTCTCAACCTACGCATTA    97

Qy    216  CAAGTGCGTTGCCTGCCAATTGCGCCACTCCAGCCAGATGCTGATGATCAACAAC      275
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     98  CAAGTGCGTTGCCTGCCAATTGCGCCACTCCAGCCAGATGCTGATGATCAACAAC      157

Qy    276  TACGAATACGTATCTTAGCGTATGTACATCACAATGAATTCGGGCGTAGAGTATCTG     335
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    158  TACGAATACGTATCTTAGCGTATGTACATCACAATGAATTCGGGCGTAGAGTATCTG     217
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Db    398  TGATGAATTGGCTGCGGAGAATTGGGCGATATTTGCTTTCTTCAGGTACGTCAAATAGTG   457
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Qy    576  ATACCAAGGTGCAAGTTCGAGCGGTGACCTCTGCGTATGGCCTGACTACTACACGCATGTGG   635

Db    458  ACACCAAGGTACAAGTTCGAGCAGTGACCATCTTCACCAACATCGGTGTGGAGAGATGCCGG   517
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    636  ATATCACGTTGAATACGATCACCATCTTCACCAACATCGGTGTGGAGAGATGCCGG     695

Db    518  ATATCACGTTGAATACGATCACCATCTTCACCAACATCGGTGTGGAGAGATGCCGG     577
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    696  TCAACGTGTTGTTCATGTGTGGGCAAGTTGGACACCAACTTCTCCAAACTGTCTGAGGTTG   755

Db    578  TCAACGTGTTTCATGTGTGGGCAAGTTGGAGGCACCAACTTCTCCAAACTGTCTGAGGTTG   637
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Qy    756  ACCGGTTTGATCCGTTCATTCAGGCGTCGTGTCACCCGCGCCTGAGGTTGCCGAGAAAATC   815

Db    638  ACCGGTTTGATCCGTTCATTCAGGCGTCGTGTCACCCGCGCCTGAGGTTGCCGAGAAAATCC  697
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    816  TGGACGAGTTGGAGCAATCGCCTGCGCGTCCTTATGGTTTCCCTGTTGCTTGGCTGGG     875

Db    698  TGGACGAGTTGGAGCAATCCCCGCGTCTTATGGTTTCCCTGTTGCTTGGCTGGG        757
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Qy    876  CAATGATGGGTGGCGCTGTTGCTGCTGTTGGGTTGGATGGTGGCAGGTTTCCCTAATTG    935

Db    758  CAATGATGGGTGGTGCTGTTGCTGCTGTTGGGTTGGATGGTGGCAGGTTTCCCTAATTG    817
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    936  CTTTTATTACCGGTCACGATCATTGCACGAGCGTCATTTTTGGGAAAGAAGGGTTTGC    995

Db    878  CTACTTTCTTCTTCCAAAATGTGTTGGTTGGTGGTTTATTGCCACGCTGCCTGCATCGATTGCTT   937
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    996  CTACTTTCTTCTTCCAAAATGTGTTGGTTGGTGGTTTATTGCCACGCTGCCTGCATCGATTGCTT  1055
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Db    818  CTTTTATTACCGGTCACGATCATTGCACGAGCGTCATTTTTGGGAAAGAAGGGTTTGC   877
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1056  ATTCTCTTTGGCGTTGCAATTTGGTCTTGAGATCAAAACCGAGCCAGCCAGATCATCGATCTGGAA  1115

Db    938  ATTCTCTTTGGCGTTGCAATTTGGTCTTGAGATCAAAACCGAGCCAGCCAGATCATCGATCTGGAA   997
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Qy   1116  TTGTTGTGCTGTTGGCAGGTTGACACTTGTGCAATCTCTGCAGGACGGCATCACGGGCG    1175

Db    998  TTGTTGTGCTGTTGGCAGGTTGACACTTGTGCAATCTCTGCAGGACGGCATCACGGGCG     1057
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Qy   1176  CTCCGGTGACAGCAAGTGCACGATTTTTGAAACACTCCTGTTTACCGGCGCATTGTTG    1235

Db   1058  CTCCGGTGACAGCAAGTGCACGATTTTGAAACACTTCCTGTTTACCGGCGCATTGTTG    1117
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1236  CTGGGCGTGGGTTTGGGCATTCAGCTTTCAGCTTTCTGCATGTCATGTCTGCCTGCCATGG   1295

Db   1118  CTGGGCGTGGGTTTGGGCATTCAGCTTTCAGCTTTCTGCATGTCATGTCTGCCTGCCATGG   1177
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1296  AGTCCCGCTGCAGCAAGTGACACCTAATTATTCGTCTACATTCGCCCGCATTATCGCCGGTGCGTCA   1355

Db   1178  AGTCCCGCTGCAGCAAGTGACACCTAATTATTCGTCTACATTCGCCCGCATTATCGCCGGTGCGTCA   1237
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1356  CCGCAGCGCGGCCCTTCGCAGTGGGTTGTTGCAGTGGGTTGTTACGCCGAGTGGTCCTCGGGTGATTATTGCGGGGC   1415

Db   1238  CCGCAGCGCGGCCCTTCGCAGTGGGTTGTTGCAGTGGGTTGTTACGCCGAGTGGTCCTCGGGTGATTATTGCGGGGC   1297
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1416  TTACTGCGCTGATGGGTTCTGCGTTTTATTACCTTCGTTGTTGTTTGTTTATTTAGGCCCCCGTCT   1475

Db   1298  TTACTGCGCTGATGGGTTCTGCGTTTTATTACCTTCGTTGTTGTTTGTTTATTTAGGCCCCCGTCT   1357
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Qy   1476  CTGCCGTCGCTGCGATTGCTGCAACAGCAGTTGGTTTCACTGGTTGGTTTCACTGGTTGGTTTGCCCGTCGAT   1535

Db   1358  CTGCCGTCGCTGCGATTGCTGCAACAGCAGTTGGTTTCACTGGTTGGTTTCACTGGTTGGTTTGCCCGTCGAT   1417
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1536  TCTTGATTCCACCGTTGATTGTGGCGATTGTGGCGGCCGCCATCACACCACCAAATGCTTCCAGGTCTAG   1595

Db   1418  TCTTGATTCCACCGTTGATTGTGGCGATTGTGGCGGCCGCCATCACACCACCAAATGCTTCCAGGTCTAG   1477
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1596  CAATTACCGCGGAATGTACGCCACCCTGAATGATCAAACACTCATGGGTTTCACCAACA   1655
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RESULT 12
US-09-951-535-3
; Sequence 3, Application US/09951535
; Publication No. US2003004980A1
; GENERAL INFORMATION:
;   APPLICANT: ZIEGLER, PETRA
;   APPLICANT: EGGELING, LOTHAR
;   APPLICANT: SAHM, HERMANN
;   APPLICANT: THIERBACH, GEORG
;   TITLE OF INVENTION: NEW NUCLEOTIDE SEQUENCES CODING FOR THE THRE GENE AND
;   TITLE OF INVENTION:  PROCESS FOR THE ENZYMATIC PRODUCTION OF L-THREONINE
;   TITLE OF INVENTION:  USING CORYNEFORM BACTERIA
;   FILE REFERENCE: 21123/282415/MAS
;   CURRENT APPLICATION NUMBER: US/09/951,535
;   CURRENT FILING DATE: 2001-09-14
;   PRIOR APPLICATION NUMBER: 09/431,099
;   PRIOR FILING DATE: 1999-11-01
;   PRIOR APPLICATION NUMBER: DE 199 41 478.5
;   PRIOR FILING DATE: 1999-09-01
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
;   LENGTH: 1909
;   TYPE: DNA
;   ORGANISM: Corynebacterium glutamicum
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (280)..(1746)
;   OTHER INFORMATION: thrE-Gen
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Qy   336 GTGAACCGTGCATAAACGACCTGTGATTGGACTCTTTTTCCTTGCAAAATGTTTTCCAGC 395
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Db   218 GTGAACCGTGCATAAACGACCTGTGATTGGACTCTTTTTCCTTGCAAAATGTTTTCCAGC 277

Qy   396 GGATGTTGAGTTTTGCGACCCCTTCGTCGCCGATTCAACAGTTGACGCTGCAAAGCCG 455
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   278 GGATGTTGAGTTTTGCGACCCCTTCGTCGCCGATTCAACAGTTGACGCTGCAAAGCCG 337

Qy   456 CACCTCCGCCATCGCCACTAGCCCCGATTGATCTCACTGACCATAGTCAAGTGGCCGGTG 515
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   338 CACCTCCGCCATCGCCACTAGCCCCGATTGATCTCACTGACCATAGTCAAGTGGCCGGTG 397

Qy   516 TGATGAATTTGGCTGCGGAGAATTGGCGATATTTGCTTTCTTCAGGTACGTCAAACAGTG 575
             |||||||||||||||||||||||||||||||||||||||| ||||||||||| |||||
Db   398 TGATGAATTTGGCTGCGGAGAATTGGCGATATTTGCTTTCTTCAGGTACGTCAAATAGTG 457

Qy   576 ATACCAAGGTGCAAGTTCGAGCGGTGACCCTCTGCGTACTATACGCATGTGG 635
             | |||||||| ||||||||||||||||||||||||||||||||||||||||
Db   458 ACACCAAGGTACAGTTCGAGCGGTGACCCTCTGCGTACTATACGCACGCTGG 517

Qy   636 ATATCACGTTGAATACGATCACCATCTTCACCAACATCGGTTGTGGAGGAAGATGCCGG 695
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   518 ATATCACGTTGAATACGATCACCATCTTCACCAACATCGGTTGTGGAGGAAGATGCCGG 577

Qy   696 TCAACGTGTTCATGTTGTGGGCAAGTTGGACACCTCTCCAAACTGTCTGAGGTTG 755
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Db   578 TCAACGTGTTTCATGTTGTGTAGGCAAGTTGGACACCAACTTCTCCAAACTGTCTGAGGTTG 637

Qy   756 ACCGTTTGATCCGTTCATTCAGGCGTCTGCCTGGCGTCTTATGGTTTCCCTGTTGCCGAGAAATTC 815
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   638 ACCGTTTGATCCGTTCATTCAGGCGTGTGCCTGGCGTCTTATGGTTTCCCTGTTGCCGAGAAATCC 697

Qy   816 TGGACGAGTTGGAGCAATCGCCTGCGTCGTGTGCGTGTTCCCTGTTGGTTGTGGTTGGCTGGG 875
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   698 TGGACGAGTTGGAGCAATCCCCTGCGTCTTATGGTTTCCCTGTTGGTTGTGGTTGGCTGGG 757

Qy   876 CAATGATGGGGTGCGCGTGTTGCTGTGTGCGTGGATGGCAGGTTTCCCTAATTG 935
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   758 CAATGATGGGGTGCGCGTGTTGCTGTGTGCGTGGATGGCAGGTTTCCCTAATTG 817

Qy   936 CTTTTATTACCGCGTTCACGATCATTGCCACGACGTCATTTTGGGAAAGAAGGGTTTGC 995
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   818 CTTTTATTACCGCGTTCACGATCATTGCCACGACGTCATTTTGGGAAGAGAGGGTTTGC 877

Qy   996 CTACTTTCTTCTTCCAAAATGTTGTGGTGTGGTTTATTGCCACCGTGCTGCATCGATTGCTT 1055
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Db   878 CTACTTTCTTCTTCCAAAATGTTGTGGTGTGGTTTATTGCCACCGTGCTGCATCGATTGCTT 937

Qy  1056 ATTCTTTGGCGTTGCAATTTGGCGTCTTGAGATCAAACCGAGCCAGATCATCGCATCTGGAA 1115
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   938 ATTCTTTGGCGTTGCAATTTGGCGTCTTGAGATCAAACCGAGCCAGATCATCGCATCTGGAA 997

Qy  1116 TTGTTGTGCTGTTGGCAGGTTTGGACACTTGTCGAATCTGTGAGACGCATCACGGGGG 1175
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   998 TTGTTGTGCTGTTGGCAGGTTTGGACACTCGTGCAATCTCTGCGAGACGGCATCACGGGGGC 1057

Qy  1176 CTCCGGTGACAGCAAGTGCACGAGATTTTTGAAACACTCCGTGTTACCGGCGGCATTGTTG 1235
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1058 CTCCGGTGACAGCAAGTGCACGATTTTTGAAACACTCCGTGTTACCGGCGGCATTGTTG 1117

Qy  1236 CTGGCGTGGGTTTGGCATTCAGCTTTCAGATCTTGAAATCTTGCATGTCATGTTGCCTGCCATGG 1295
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1118 CTGGGCGTGGGTTTGGCATTCAGCTTTCAGATCTTGAAATCTTGCATGTCATGTTGCCTGCCATGG 1177

Qy  1296 AGTCCGCTGCAGCAAGTGCACCTTAATTATTCGTCTACATTCGCCCGCCATTATCGTTGGTGGCGTCA 1355
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1178 AGTCCGCTGCAGCAAGTGCACCTTAATTATTCGTCTACATTCGCCCGCCATTATCGCTGTGGCGTCA 1237

Qy  1356 CCGCAGCGGCCTTCGCCAGTGGGTTGGTTACGCGGAGTGGTCCTCGGTGATTATTGCGGGGC 1415
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1238 CCGCAGCGGCCTTCGCCAGTGGGTTGGTTACGCGGAGTGGTCCTCGGTGATTATTGCGGGGC 1297

Qy  1416 TTACTGCGCGTGATGGGGTTCTCGGTTTATTACCTCTTCGTTGTTGTTATTGTTATTGGGCCCCCGTCT 1475
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Db  1298 TTACTGCGCTGCGATGGGGTTCTCGGTGTTATTACCTCTTCGTGTGTTGTTATTGAGGGCCCCGTGTCT 1357

Qy  1476 CTGCGCCGTGCGGATTGCTGCAACAGCAGTGGTTCACTGGTTGCTTCGTCGTGGTTGCCCGTCGAT 1535
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Db  1358 CTGCCGCTGCGGATTGCTGCAACAGCAGTGGTTCACTGGTTGCTTCGTCGTGGTTGCCCGTCGCT 1417

Qy  1536 TCTTGATTCCACCGTTGATTGTTGGCGGATTGCCGGCATCACACCACCAATGCTTCAGGTCTAG 1595
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Db  1418 TCTTGATTCCACCGTTGATTGTTGGCGGATTGCCGGCATCACACCACCAATGCTTCAGGTCTAG 1477

Qy  1596 CAATTTACCGCGGAATGTACGCGCCACCTTGAATGATCAAACACTCATGGTTTCACCAACA 1655
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Db  1478 CAATTTACCGCGGAATGTACGCGCCACCCTGAATGATCAAACACTCATGGTTTCACCAACA 1537

Qy  1656 TTGCGGTTGCTTAGCCACTGCTTCATCACTGCTTCATCACTTGCCGCCGTGGCGTGGTTTGGGTGAGTGGA 1715
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1538 TTGCGGTTGCTTAGCCACTGCTTCATCACTGCTTCATCACTGCCGCCGTGGCGTGGTTTGGGTGAGTGGA 1597

Qy  1716 TTGCCCGGAGGCTACGTGCTCGTCCAACCAGGCTTCAACCAGTAACCCATACCGTGCATTACCAAGGCGA 1775
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1598 TTGCCCGGAGGCTACGTGCTCGTCCAACCAGGCTTCAACCACGCTCCATACCCGTGCATTACCAAGGCGA 1657

Qy  1776 ATGAGTTCTCCTTCCAGGAGGAAGCTGAGCAGGAAGCTGTAATAAAAATCAACCTGCTCTTCGCT 1835
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Db  1658 ATGAGTTCTCCTTCCAGGAGGAAGCTGAGCAGGAAGCTGTAATAAAAATCAACCTGCTCTTCGCT 1717

Qy  1836 AGACTAATCAAAGATTCGGTAGAATATCGGGTCGATCGTGCTTTTAAACACTCAGGAGGA 1895
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1718 AGACTAATCAGAATTCGGTAGAATATCGGGTCGATCCGTTTTAAACACTCAGGAGGA 1777

Qy  1896 TAAATAGCGTAGAATATCGGGTCGATCCCAACCCCAGAATCCCTTCACGCTGTTGAAGAGGAAACCGCCA 1955
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1778 TAAATAGCGTAGAATATCGGGTCGATCCGTTTTAAACACTCAGAATCCCTGCCGCC 1837

Qy  1956 AAAATCACGGACACTCGTCCCACCCCAGAATCCCTTCACGCTGTTGAAGAGGAAACCGCCA 2015
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1838 AAAATCACGGACACTCGTCCCACCCCAGAATCCCTTCACGCTGTTGAAGAGGAAACCGCCA 1897

Qy  2016 GCCGGTG 2022
             |||||||
Db  1898 GCCGGGG 1904
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US-09-951-535-3

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Query Match      65.2%;   Score 1836.6;   DB 10;   Length 1909;
Best Local Similarity  99.0%;   Pred. No. 0;   Gaps   0;
Matches 1848;   Conservative   0;   Mismatches   19;   Indels   0;   Gaps   0;

Qy     156 CCCCTTTGACCTGGTGTATTGAGCTGGAGAAGAGACTTGAACTCTCAACCTACGCATTA 215
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      38 CCCCTTTGACCTGGTGTATTGAGCTGGAGAAGAGACTTGAACTCTCAACCTACGCATTA 97

Qy     216 CAAGTGCGTTGCGCTGCCAATTGCGCCACTCCAGCACCGCAGATGTCTGATGATCAACAAC 275
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      98 CAAGTGCGTTGCGCTGCCAATTGCGCCACTCCAGCACCGCAGATGTCTGATGATCAACAAC 157

Qy     276 TACGAATACGTATCTTAGCGTATGTGTACATCACAATGGAATTCGGGGCTAGAGTATCTG 335
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     158 TACGAATACGTATCTTAGCGTATGTGTACATCACAATGGAATTCGGGGCTAGAGTATCTG 217

Qy     336 GTGAACCGTGCATAAACGACCTGATTGGACTCTTTTCCTTGCAAAATGTTTTCCAGC 395
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     218 GTGAACCGTGCATAAACGACCTGATTGGACTCTTTTCCTTGCAAAATGTTTTCCAGC 277

Qy     396 GGATGTTGAGTTTTGCGACCCTTCGTGGCCGATTTCAACAGTTGACGCTGCAAAAGCCG 455
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     278 GGATGTTGAGTTTTGCGACCCTTCGTGGCCGATTTCAACAGTTGACGCTGCAAAAGCCG 337

Qy     456 CACCTCCGCCATCGCCACTAGCCCCGATTGATCTCACTGACCATAGTCAAGTGGCCGGTG 515
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     338 CACCTCCGCCATCGCCACTAGCCCCGATTGATCTCACTGACCATAGTCAAGTGGCCGGTG 397

Qy     516 TGATGAATTGGCTGCGGAGAATTGGCCGATATTTGCTTTCTTCAGGTACGTCAAACAGTG 575
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     398 TGATGAATTGGCTGCGGAGAATTGGCCGATATTTGCTTTCTTCAGGTACGTCAAATAGTG 457

Qy     576 ATACCAAGGTGCAAGTTCGAGCGGTGACCTCTGCGTATGGCCTGTACTATACGCATGTGG 635
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     458 ACACCAAGGTACAAGTTCGAGCGGTGACCTCTGCGTACGGTTTGTACTACACGCACGTGG 517

Qy     636 ATATCACGTTGAATACGATCACCATCTTCACCAACATCGGTGTGGAGGAAGATGCCGG 695
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     518 ATATCACGTTGAATACGATCACCATCTTCACCAACATCGGTGTGGAGGAAGATGCCGG 577

Qy     696 TCAAGTGTTTCATGTGTGGGCAAGTTGACACCAACTTCTCCAAACTGTCTGAGGTTG 755
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     578 TCAAGTGTTTCATGTGTGGGCAAGTTGACACCAACTTCTCCAAACTGTCTGAGGTTG 637

Qy     756 ACCGGTTTGATCCGTTCATTCAGGCTGGTGCTACCCCGCCTGAGGTTGCCGAGAAAATTC 815
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     638 ACCGGTTTGATCCGTTCATTCAGGCTGGTGCTACCCCGCCTGAGGTTGCCGAGAAATCC 697

Qy     816 TGGACGAGTTGGAGCAATCGCCTCGGCTCTTATGGTTTCCCTGTGCTTGGCGTGGGG 875
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     698 TGGACGAGTTGGAGCAATCGCCTCGGCTCTTATGGTTTCCCTGTGCTTGGCGTGGGG 757

Qy     876 CAATGATGGGTGGCGCGTGTTGCGCGTGTTGGGTGGATGGCAGTTTCCCTAATTG 935
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     758 CAATGATGGGTGGCGCGTGTTGCGCGTGTTGGGTGGATGGCAGTTTCCCTAATTG 817

Qy     936 CTTTTATTACCGCGTTCACGATCATTGCCACGACGTCATTTTTGGGAAAGAAGGGTTTGC 995
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Db     818 CTTTTATTACCGCGTTCACGATCATTGCCACGACGTCATTTTTGGGAAAGAAGGGTTTGC 877

Qy     996 CTACTTTCTTCAAAATGTTGTTGGTGGTTGGTTTATTGCCACGCGTGCCGCCATCGGAA 1055
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     878 CTACTTTCTTCAAAATGTTGTTGGTGGTTGGTTTATTGCCACGCGTGCCGCCATCTGCTT 937

Qy    1056 ATTCTTTGGCGTTCAATTTGGTTCTTGAGATCAAACCGAGCCAGATCAAACGGAA 1115
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Db     938 ATTCTTTGGCGTTCAATTTGGTTCTTGAGATCAAACCGAGCCAGATCATCGGAA 997

Qy    1116 TTGTTGCTGTTGGCAGGTTTGGCAGGTTTGACACTTGTCAATCTCTGCAGGACGGCATCACCGGGCG 1175
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     998 TTGTTGCTGTTGGCAGGTTTGGCAGGTTTGACACTTGTCAATCTCTGCAGGACGGCATCACCGGGCG 1057
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Qy    1176 CTCCGGTGACAGCAGCAAGTGCACGATTTTTGAAACACTCCTGTTTACCGGCGGCATTGTG 1235
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1058 CTCCGGTGACAGCAGCAAGTGCACGATTTTTGAAACACTCCTGTTTACCGGCGGCATTGTG 1117

Qy    1236 CTGGCGTGGGTTGGGCATTCAGCTTTCTGAAATCTTCTGAAATCTTGCCTGCCATGG 1295
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Db    1118 CTGGCGTGGGTTGGGCATTCAGCTTTCTGAAATCTTCTGAAATCTTGCCTGCCATGG 1177

Qy    1296 AGTCCGCTGCAGCACTTAATTATTCGTCACAGTTCGCCCGCATTATCGCTGGTGGCGTCA 1355
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1178 AGTCCGCTGCAGCACTTAATTATTCGTCACAGTTCGCCCGCATTATCGCTGGTGGCGTCA 1237

Qy    1356 CCGCAGCGGCCTTCGCAGTGGGTTGTACGGCGGAGTGGTCCTCGGTGATTATTGCGGGGC 1415
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1238 CCGCAGCGGCCTTCGCAGTGGGTTGTACGGCGGAGTGGTCCTCGGTGATTATTGCGGGGC 1297

Qy    1416 TTACTGCCGATGGGTTCTCGCGTTTATTACCTTCGTGTTGTTATTTAGGCCCCGTCT 1475
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1298 TTACTGCCGATGGGTTCTCGCGTTTATTACCTTCGTGTTGTTATTTAGGCCCCGTCT 1357

Qy    1476 CTGCCGCTGCGATTGCTGCAACAGCAGTTGGTTTCACTGGTGGTTTGCCTGCCGTCGAT 1535
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1358 CTGCCGCTGCGATTGCTGCAACAGCAGTTGGTTTCACTGGTGGTTTGCCTGCCGTCGAT 1417

Qy    1536 TCTTGATTCCACCGTGATTGTGGCGATTGCCGGCATCACACCAAATGCTTCCAGGTCTAG 1595
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1418 TCTTGATTCCACCGTGATTGTGGCGATTGCCGGCATCACACCAAATGCTTCCAGGTCTAG 1477

Qy    1596 CAATTTACCTGCGGAATGTACGCACCTGAATGCATCATGTTTCACCAACA 1655
           ||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1478 CAATTTACCTGCGGAATGTACGCACCTGAATGCATCATGTTTCACCAACA 1537

Qy    1656 TTGCGGTTGCTTTAGCCACTGCTTCATCACTTGCCGCTGGGTGTTTGGGTGAGTGGA 1715
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1538 TTGCGGTTGCTTTAGCCACTGCTTCATCACTTGCCGCTGGGTGTTTGGGTGAGTGGA 1597

Qy    1716 TTGCCCGAGGCTACGTCGTCAACCATACCGTCATTTACCAAGGCGA 1775
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Db    1598 TTGCCCGAGGCTACGTCGTCAACCATACCGTCATTTACCAAGGCGA 1657

Qy    1776 ATGAGTTCTCCTTCCAGGAGGAAGCTGAGCAGAATCAGGCGCCGGCAGAAAAGTCCAA 1835
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1658 ATGAGTTCTCCTTCCAGGAGGAAGCTGAGCAGAATCAGCCGCCGGCAGAAAAACGTCCAA 1717

Qy    1836 AGACTAATCAAAGATTCGGTAATAAAATCAACCTGCTCTTTGCT 1895
           ||||||||||||||||||||||||||||||||||||||||||||
Db    1718 AGACTAATCAGAGATTCGGTAATAAAATCAACCTGCTCTTTCGCT 1777

Qy    1896 TAAATAGGCTAGAATATCGGGTGATCGCTTTAAACACTCAGGAGGATCCTTGCCGGCC 1955
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1778 TAAATAGCCTAGAATATCGGGTCGATCGCTTTAAACACTCAGGAGGATCCTTGCCGCC 1837

Qy    1956 AAAATCACGGACACTCGTCCCACCCCAGAATCCCTTCACGCTGTGAAGAGAACCGCA 2015
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Db    1838 AAAATCACGGACACTCGTCCCACCCCAGAATCCCTTCACGCTGTGAAGAGAACCGCA 1897

Qy    2016 GCCGGTG 2022
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Db    1898 GCCGGGG 1904
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;  CURRENT APPLICATION NUMBER: US/10/224,574
;  CURRENT FILING DATE: 2002-08-21
;  SOFTWARE: PatentIn Ver. 2.1
;  SEQ ID NO 11
;  LENGTH: 1909
;  TYPE: DNA
;  ORGANISM: C. glutanicum ATCC 13 032
;  FEATURE:
;  NAME/KEY: CDS
;  LOCATION: (280)...(1746)
;  OTHER INFORMATION: thr E  (Threonin-exportcarrier)
US-10-224-574-11

Query Match        65.2%;  Score 1836.6;  DB 17;  Length 1909;
Best Local Similarity  99.0%;  Pred. No. 0;
Matches 1848;  Conservative  0;  Mismatches  19;  Indels  0;  Gaps  0;

Qy   156 CCCCTTTGACCTGGTGTTGTTATTGAGCTGGAAGAGAGACTTGAACTCTCAACCTACGCATTA 215
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Db    38 CCCCTTTGACCTGGTGTTGTTATTGAGCTGGAAGAGAGACTTGAACTCTCAACCTACGCATTA 97

Qy   216 CAAGTGCGTTGCGCTGCCAATTGGGCCACTCCAGCACCGCAGATGCTGATGATCAACAAC 275
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    98 CAAGTGCGTTGCGCTGCCAATTGGGCCACTCCAGCACCGCAGATGCTGATGATCAACAAC 157

Qy   276 TACGAATACGTATCTTAGCGTATGTGTACATCACAATGGAATTCGGGGCTAGAGTATCTG 335
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   158 TACGAATACGTATCTTAGCGTATGTGTACATCACAATGGAATTCGGGGCTAGAGTATCTG 217

Qy   336 GTGAACACCGTGCATAAACGACCTGATTGGACTCTTTTCCTTGCAAAATGTTTTCCAGC 395
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Db   218 GTGAACACCGTGCATAAACGACCTGATTGGACTCTTTTCCTTGCAAAATGTTTTCCAGC 277

Qy   396 GGATGTTGAGTTTTGCGACCCTTCGTGCCGCATTCAACAGCAGTTGGTCTTGACGCTGCAAAAGCCG 455
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Db   278 GGATGTTGAGTTTTGCGACCCTTCGTGCCGCATTCAACAGCAGTTGGTCTTGACGCTGCAAAAGCCG 337

Qy   456 CACCTCCGCCATCGCCTACTAGCCCCGATTGATCTCCACTGACCATAGTCAAGTGGCCGGTG 515
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Db   338 CACCTCCGCCATCGCCTACTAGCCCCGATTGATCTCCACTGACCATAGTCAAGTGGCCGGTG 397

Qy   516 TGATGAATTTGGCTGCGGAGAATTGGCGATATTTGCTTTCTTCAGGTACGTCAAACAGTG 575
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   398 TGATGAATTTGGCTGCGGAGAATTGGCGATATTTGCTTTCTTCAGGTACGTCAAACAGTG 457

Qy   576 ATATCCAAGGTGCAAGTTCGAGCGGGTGACCTCGTGCGTATACTATACGCATGTGG 635
             |||||||||     |||||||||||||||||||||||||||||||||||||||||||||
Db   458 ACACCAAGGTACAAGTTCGAGCAGTTCGAGCGGGTGACCTCGTGCGTATACTATACGCACGTGG 517

Qy   636 ATATCACGTTGAATACGATCACCATCTTCACCAAACATCGGTGTGGAGGAAGATGCCGG 695
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   518 ATATCACGTTGAATACGATCACCATCTTCACCAAACATCGGTGTGGAGGAAGATGCCGG 577

Qy   696 TCAACGTGTTTCATGTTGTGGGCAAGTTGGACACCAAACTTCTCCAAACTGTCTGAGGTTG 755
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   578 TCAACGTGTTTCATGTTGTGGGCAAGTTGGACACCAAACTTCTCCAAACTGTCTGAGGTTG 637

Qy   756 ACCGGTTGATCCGTTCCATTCAGGCTGGTGCTACCCGCCGCTGGTGCTACCCGCCGCTGGTTGCCGAGAAATTC 815
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Qy   816 TGGACCAGTTGGAGCAATCGCCTGCGGTCTTATGGTTTCCCTGTTGCGTTGCTGGGG 875
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Db   698 TGGACCAGTTGGAGCAATCCCCTGCGGTCTTATGGTTTCCCTGTTGCGTTGCTTGGCTGGGG 757

Qy   876 CAATGATGGGTTGGCGCTGTTGTCTGTTGGTGGTGATGGCGAGGTTTCCCTAATTG 935
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Db   758 CAATGATGGGTTGGCGTCGTTGTGTCTGTTGGGGTGATGGCAGGTTTCCCTAATTG 817

Qy   936 CTTTTATTACCGCCGTTCACGATCANTTGCCACGACGTCATTTTTTGGGAAAGAAAGGGTTTGC 995
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Db   818 CTTTTATTACCGCCGTTCACGATCANTTGCCACGACGTCATTTTTTGGGAAAGAAAGGGTTTGC 877
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Qy   996 CTACTTTCTTCCAAAATGTTGGTGGTTTATTGCCAACGTCGCCTGCCTGATTGCTT 1055
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Qy  1056 ATTCTTTGGCGTTGCAATTGGTCTTGAGATCAAACCGAGCCAGATCATCGCATCTGAA 1115
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Qy  1116 TTGTTGTCGTGGCAGGTTGACACTTGTGCAATCTGCGTGACGACGGCGCATCACGGGCG 1175
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Db   998 TTGTTGTCGTGGCAGGTTGACACTCGTGCAATCTCTGCGTGACGACGGCGCATCACGGGCG 1057

Qy  1176 CTCCGGTGACAGCAAGTGCACGATTTTTGAAACACTCCGTGTTACCGCGGCATTGTTG 1235
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Db  1058 CTCCGGTGACAGCAAGTGCACGATTTTTCGAAACACTCCGTGTTACCGCGGCATTGTTG 1117

Qy  1236 CTGGCGTGGGTTGGGCATTCAGCTTTCTGAAATCTTCTGAAATCTTGCATGTGCCTGCCATGG 1295
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Db  1118 CTGGCGTGGGTTGGGCATTCAGCTTTCTGAAATCTTCTGAAATCTTGCATGTGCCTGCCATGG 1177

Qy  1296 AGTCCGCTGCAGCACCTAATTATTCGTCTACATTCGCCGCATTATCGCTGCTGGGCGTCA 1355
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1178 AGTCCGCTGCAGCACCTAATTATTCGTCTACATTCGTCTACATTCGCCGCATTATCGCTGTGGGCGTCA 1237

Qy  1356 CCGCAGCGGCCTTCGCGAGTGGTTGTTACGGGAGTGGTCTCGGTGATTATTGCGGGGC 1415
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Db  1238 CCGCAGCGGCCTTCGCGAGTGGTTGTTACGGGAGTGGTCTCGGTGATTATTGCGGGGC 1297

Qy  1416 TTACTGCGCTGATGGGTTCTGCGTTTATTAGGCCCGTCT 1475
             ||||||||||||||||||||||||||||||||||||||
Db  1298 TTACTGCGCTGATGGGTTCTGCGTTTATTACCTCTTCGTTGTTTATTAGGCCCGTCT 1357

Qy  1476 CTGCCGCTGCGATTGCTGCAACAGCAGTTGGTTTCACTGGGTGGTTTGCTTGCCGTCGAT 1535
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Db  1358 CTGCCGCTGCGATTGCTGCAACAGCAGTTGGTTTCACTGGGTGGTTTGCTTGCCCGTCGAT 1417

Qy  1536 TCTTGATTCCACCGTTGATTGTGGCGATTGCGCGGCATCACCACCAATGCTTCCAGTCTAG 1595
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Db  1418 TCTTGATTCCACCGTTGATTGTGGCGATTGCGCGGCATCACCACACCAATGCTTCCAGTCTAG 1477

Qy  1596 CAATTTACCGGCGAATGTACGGCCACCTTGAATGATCAAAACACTCATGGGTTCACCAACA 1655
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Db  1478 CAATTTACCGGCGAATGTACGGCCACCTTGAATGATCAAAACACTCATGGGTTCACCAACA 1537

Qy  1656 TTGCGGTTGCTTAGCCACTGCTTCATCACTTGCGCGCTGGGCGTGGGTTTGGGTAGTGGA 1715
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Db  1538 TTGCGGTTGCTTAGCCACTGCTTCATCACTTGCGCGCTGGGCGTGGGTTTGGGTAGTGGA 1597

Qy  1716 TTGCCCAGGCTAGCTGCGTCCAACCAGCTTCAACCCATACGTGCATTACCAAGGGCGA 1775
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Db  1598 TTGCCCAGGCTAGCTGCGTCCAACCAGCTTCAACCCATACGTGCATTACCAAGGGCGA 1657

Qy  1776 ATGAGTTCTCCTTCCAGGAGGAAGCTGAGCGAGTCAATCAGCGCCGCCGAGAAAACGTCCAA 1835
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Db  1658 ATGAGTTCTCCTTCCAGGAGGAAGCTGAGCGAGTCAATCAGCGCCGCCGAGAAAAGTCCAA 1717

Qy  1836 AGACTAATCAAAGATTCGGTAATAAAGGTAAAAATCAACCTGCTCTTTCGCT 1895
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Db  1718 AGACTAATCAGAGATTCGGTAATAAAGGTAAAAATCAACCTGCTCTTTCGCT 1777

Qy  1896 TAAAATAGGCGTAGAATATCGGGTCGATCGGTTTTTAAACACTCAGGAGGAACCGGCC 1955
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Db  1778 TAAAATAGGCGTAGAATATCGGGTCGATCGGTTTTTAAACACTCAGGAGGAACCGGCC 1837

Qy  1956 AAAATCACCGACACTCGTCCACCCCAGAATCCCTTCACGCGTGTTGAGAGGAACCGGCA 2015
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Db  1838 AAAATCACCGACACTCGTCCACCCCAGAATCCCTTCACGCGTGTTGAGAGGAACCGCA 1897

Qy  2016 GCCGGTG 2022
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Db  1898 GCCGGGG 1904
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RESULT 14
US-10-627-476-557
; Sequence 557, Application US/10627476
; Publication No. US20040030116A1
; GENERAL INFORMATION:
; APPLICANT: Pompejus, Mark
; APPLICANT: Kroger, Burkhard
; APPLICANT: Schoder, Hartwig
; APPLICANT: Zelder, Oskar
; APPLICANT: Haberhauer, Gregor
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS
; TITLE OF INVENTION: INVOLVED IN MEMBRANE SYNTHESIS AND MEMBRANE
; TITLE OF INVENTION: TRANSPORT
; FILE REFERENCE: BGI-125CPCN
; CURRENT APPLICATION NUMBER: US/10/627,476
; CURRENT FILING DATE: 2003-07-25
; PRIOR APPLICATION NUMBER: 09/602,787
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: USSN 60/141031
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: DE 19931454.3
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931478.0
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931563.9
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19932122.1
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932124.8
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932125.6
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932128.0
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932180.9
; PRIOR FILING DATE: 1999-07-09
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 678
; SEQ ID NO 557
; LENGTH: 1590
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (101)..(1567)
; OTHER INFORMATION: RXN00349
US-10-627-476-557

Query Match   55.4%; Score 1561.2; DB 16; Length 1590;
Best Local Similarity   98.9%; Pred. No. 0;
Matches 1572; Conservative   0; Mismatches 18; Indels   0; Gaps   0;

Qy   298 TGTGTACATCACAATGAGAATTCGGGCTAGAGTATCGGGCTAGACGTGACCGTGCATAAACGACCT 357
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Qy   358 GTGATTGGACTCTTTTCCTTGCAAAATGTTTCCAGCGGATGTGAGTTTTGCGACCCT 417
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 GTGATTGGACTCTTTTCCTTGCAAAATGTTTCCAGCGGATGTGAGTTTTGCGACCCT 120

Qy   418 TCGTGGCCGCATTTCAACAGTTGACGCTGCAAAAGCCGCACCTCCGCCATCGCCACTAGC 477
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 TCGTGGCCGCATTTCAACAGTTGACGCTGCAAAAGCCGCACCTCCGCCATCGCCACTAGC 180

Qy   478 CCCGATTGATCTCACTGACCATAGTAGTCAAGTGCCGGTGTGATGAATTGGCGTGCGAGAAT 537
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 CCCGATTGATCTCACTGACCATAGTAGTCAAGTGCCGGTGTGATGAATTGGCGTGCGAGAAT 240

Qy   538 TGGCGATATTTTGCTTTCTTCAGGTACGTCAAACAGTGATACCAAGGTGCAAGTTCGAGC 597
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 TGGCGATATTTTGCTTTCTTCAGGTACGTCAAATAGTGACACCAAGGTACAAGTTCGAGC 300

Qy   598 GGTGACCTCTGCGTATGGCCGTGCTACTATACGCATGTGGATATCACGTTGAATACGATCAC 657
                |||||||| ||||||||| ||||||||||||||| ||||||||||||||||||||||
Db   301 AGTGACCTCTGCGTACGGTTTGTACTACACGCACGTGGATATCACGTTGAATACGATCAC 360

Qy   658 CATCTTCACCAACATCGGTGTGGAGAGGAAGATGCCGGTCAACGTGTTCATGTTGTGGG 717
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 CATCTTCACCAACATCGGTGTGGAGAGGAAGATGCCGGTCAACGTGTTCATGTTGTAGG 420

Qy   718 CAAGTTGGACACCAACTTCTCCAAACTGTCTGAGGTTGACCGTTTGATCCGTTCCATTCA 777
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 CAAGTTGGACACCAACTTCTCCAAACTGTCTGAGGTTGACCGTTTGATCCGTTCCATTCA 480

Qy   778 GGCTGGTGCTACCCCGCCTGAGCTTGCCGAGAAAATTCTGGACGAGTTGGAGCAATCGCC 837
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Db   481 GGCTGGTGCTACCCCGCCTGAGCTTGCCGAGAAAATCCTGGACGAGTTGGAGCAATCCCC 540

Qy   838 TGGCGTCTTATGGTTTCCCTGTTGCTTGGCTGGGCAATGATGAGGGCGCTGTGC 897
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Qy   1138 GACACTTGTGCAATCTCTGCAGGACGCCATCACCGGGGCTCCGGTGACGCAAGTGCACG 1197
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Qy   1198 ATTTTTGAAACACTCCTGTTTACCGGCGCCATTGTTGCTGGGGTTGGGCATTCA 1257
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Qy   1258 GCTTTCTGAAATCTTGCATGTCATGTTGCCTGCGCCATGGAGTCCGCTGCAGCACCTAATTA 1317
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Qy   1318 TTCGTCTACATTCGCCCGCCATTATCGCTGGTGGCGTCACCGCGGGGCCTTCGCAGTGGG 1377
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Qy   1378 TTGTTACCGGAGTGGTCCTCGGTGATTATTGCGGGGTTCGCTGATGGGGTTCTGC 1437
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Qy   1678 TTCATCACTTGCCCGCTGGCGTGGTTTTCGGGTGAGTGAGGTTTTCGGGTACGTCGTCC 1737

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Qy   778  GGCTGGTGCTGCTACCCGCCTGAGGTTGCCGAGAAAATTCTGGACGAGTTGGAGCAATCGCC   837
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Db   481  GGCTGGTGCTGCGACCCGCCTGAGGTTGCCGAGAAAATCTGGACGAGTTGGAGCAATCCCC    540

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RESULT 15
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; Sequence 41, Application US/10450055
; Publication No. US20040043953A1
; GENERAL INFORMATION:
; APPLICANT: BASF Aktiengesellschaft
; TITLE OF INVENTION: No. US20040043953A1el genes of Corynebacterium
; FILE REFERENCE: 936_2000
; CURRENT APPLICATION NUMBER: US/10/450,055
; CURRENT FILING DATE: 2003-06-10
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn Vers. 2.0
; SEQ ID NO 41
; LENGTH: 1590
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (101)..(1567)
; OTHER INFORMATION: RXS00349
US-10-450-055-41

Query Match   55.4%; Score 1561.2; DB 16; Length 1590;
Best Local Similarity 98.9%; Pred. No. 0;
Matches 1572; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

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Job time : 1549.15 secs

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Sun Jan 16 16:11:36 2005

us-09-963-521-3.rni

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          Copyright  GenCore version 5.1.6
          Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on:        January 14, 2005, 08:54:47 ; Search time 163.998 Seconds
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Perfect score: 1909
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Scoring table: IDENTITY_NUC
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Searched:      824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters:      1649014

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
                 Maximum Match 100%
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	1909	100.0	1909	4	US-09-431-099-3	Sequence 3, Appli
2	1836.6	96.2	2817	4	US-09-431-099-1	Sequence 1, Appli
3	1590	83.3	1590	4	US-09-602-787A-557	Sequence 557, App
4	86.6	4.5	4403765	3	US-09-103-840A-2	Sequence 2, Appli
5	86.6	4.5	4411529	3	US-09-103-840A-1	Sequence 1, Appli
6	47.6	2.5	7218	1	US-08-232-463-14	Sequence 14, Appl
7	46.6	2.4	400	4	US-08-956-171E-4234	Sequence 4234, Ap
8	46.6	2.4	400	4	US-08-781-986A-4234	Sequence 4234, Ap
9	45.8	2.4	1230025	4	US-09-198-452A-1	Sequence 1, Appli
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38	42	2.2	339	4	US-08-956-171E-4263	Sequence 4263, Ap
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ALIGNMENTS

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US-09-431-099-3
; Sequence 3, Application US/09431099
; Patent No. 6410705
; GENERAL INFORMATION:
;  APPLICANT:  Degussa-Hüls AG
;  APPLICANT:  Forschungszentrum-Jülich GmbH
;  TITLE OF INVENTION:  New nucleotide sequences coding for the thrE gene and process fo
;  TITLE OF INVENTION:  enzymatic production of L-threonine with coryneform bacteria.
;  FILE REFERENCE:  990079 BT
;  CURRENT APPLICATION NUMBER:  US/09/431,099
;  CURRENT FILING DATE:  1999-11-01
;  NUMBER OF SEQ ID NOS:  4
;  SOFTWARE:  PatentIn Ver. 2.1
;
; SEQ ID NO 3
;  LENGTH: 1909
;  TYPE: DNA
;  ORGANISM: Corynebacterium glutamicum ATCC13032
;  FEATURE:
;  NAME/KEY: CDS
;  LOCATION: (280)..(1746)
;  OTHER INFORMATION: thrE-Gen
US-09-431-099-3

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Best Local Similarity   100.0%;  Pred. No. 0;
Matches 1909;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Qy    421 GGGCGATATTTGCTTTCTTCAGGTACGTCAAATAGTGACACCAAGGTACAAGTTCGAGCA 480
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 GGGCGATATTTGCTTTCTTCAGGTACGTCAAATAGTGACACCAAGGTACAAGTTCGAGCA 480
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Qy    481 GTGACCTCTGCGTACGGTTGTACTACACGCACGTGGATATCACGTTGAATACGATCACC 540
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 GTGACCTCTGCGTACGGTTGTACTACACGCACGTGGATATCACGTTGAATACGATCACC 540
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```
Qy    541 ATCTTCACCAAACATCGGTGTGGAAGAGATGCCGGTCAACGTGTTCATGTTGTAGGC 600
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 ATCTTCACCAAACATCGGTGTGGAAGAGATGCCGGTCAACGTGTTCATGTTGTAGGC 600
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Qy    601 AAGTTGGACACCAACTCTCCAAACGTCTGAGGTTGACCGTTTGATCCGTTCCATTCAG 660
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 AAGTTGGACACCAACTCTCCAAACGTCTGAGGTTGACCGTTTGATCCGTTCCATTCAG 660
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Qy    661 GCTGGTGCGACCCGCCTGAGGTTGCCGAGAAATCCTGGACGAGTTGGAGCAATCCCCT 720
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 GCTGGTGCGACCCGCCTGAGGTTGCCGAGAAATCCTGGACGAGTTGGAGCAATCCCCT 720
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Qy    721 GGCTCTTATGGTTCCCTGGTTGGCTGGCGCAATGAATGGTGGTGGTGCTGTTGCT 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 GGCTCTTATGGTTCCCTGGTTGGCTGGCGCAATGAATGGTGGTGGTGCTGTTGCT 780
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Qy    781 GTGCTGTTGGGTGGTGGATGGCAGGTTCCCTAATTGCTTTTATTACCGCGTTCACGATC 840
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 GTGCTGTTGGGTGGTGGATGGCAGGTTCCCTAATTGCTTTTATTACCGCGTTCACGATC 840
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Qy    841 ATTGCCACGACGTCATTTTGGGAAAGAAGGGTTTGCCTACTTTCTTCTTTGGCGTTGTT 900
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 ATTGCCACGACGTCATTTTGGGAAAGAAGGGTTTGCCTACTTTCTTCTTTGGCGTTGTT 900
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Qy    901 GGTGGTTTATTGCCACGCTGCCTGCCTGCATCGATTGCTTATTCTTGCGTTGCAATTGGT 960
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 GGTGGTTTATTGCCACGCTGCCTGCCTGCATCGATTGCTTATTCTTGCGTTGCAATTGGT 960
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Qy    961 CTTGAGATCAAACCGAGCCAGCCAGATCATCGCCATCTGGAATTGTGTGCGTGTTGGCAGGTTG 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961 CTTGAGATCAAACCGAGCCAGCCAGATCATCGCCATCTGGAATTGTGTGCGTGTTGGCAGGTTG 1020
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Qy   1021 ACACTCGTGCAATCTCTGCAGACGGCGATCACGGGCGCTCCGGTGACAGCAAGTGCACGA 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 ACACTCGTGCAATCTCTGCAGACGGCGATCACGGGCGCTCCGGTGACAGCAAGTGCACGA 1080
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Qy   1081 TTTTTCGAAAACACTCCGTGTTACCGGCGCATTGTTGCTGCGGCGTGGGTGGCATTCAG 1140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 TTTTTCGAAAACACTCCGTGTTACCGGCGCATTGTTGCTGCGGCGTGGGTGGCATTCAG 1140
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Qy   1141 CTTTCTGAAATCTTGCATGTCATGTGCTCGCTGCCATGGAGTCCGCTGAGCACCTAATTAT 1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141 CTTTCTGAAATCTTGCATGTCATGTGCTCGCTGCCATGGAGTCCGCTGAGCACCTAATTAT 1200
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Qy   1201 TCGTCTACATTCGCCCGCATTATCGCTGGTGCGTCACCGCAGCCGCCTTCGCAGTGGGT 1260
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Db   1201 TCGTCTACATTCGCCCGCATTATCGCTGGTGCGTCACCGCAGCCGCCTTCGCAGTGGGT 1260
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Qy   1261 TGTTACGGCGGAGTGGTGCTCCGTGATTAATTGCGCGCTGACTCGCTGATGGGTTCGCG 1320
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1261 TGTTACGGCGGAGTGGTGCTCCGTGATTAATTGCGCGCTGACTCGCTGATGGGTTCGCG 1320
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Qy   1321 TTTTATTTACCTTCTGTTGTTTATTAGGCCCGTCTCTGCGCTGCGATTGCTGCAACA 1380
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Db   1321 TTTTATTTACCTTCTGTTGTTTATTAGGCCCGTCTCTGCGCTGCGATTGCTGCAACA 1380
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Qy   1381 GCAGTTGGTTTCACTGGTGGTTGCTTGCCCGTGATTCTTGATTCTTCACCGTTGATTGTG 1440
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Db   1381 GCAGTTGGTTTCACTGGTGGTTGCTTGCCCGTGATTCTTGATTCTTCACCGTTGATTGTG 1440
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Qy   1441 GCGATTGCCGGCATCACACCAATGCTTCCAGGTCTAGCAATTTACCGCGGCGAATGTACGCC 1500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1441 GCGATTGCCGGCATCACACCAATGCTTCCAGGTCTAGCAATTTACCGCGGCGAATGTACGCC 1500
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Qy   1501 ACCTGAATGATCAAAACATTGGTTTCACCAACACATTGCGGTTGCTTTAGCCACTGCT 1560
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Db   1501 ACCTGAATGATCAAAACATTGGTTTCACCAACACATTGCGGTTGCTTTAGCCACTGCT 1560
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Qy   1561 TCATCACTTGCCGCTGGCGTGGTTTGGGTGAGTGGATTGCCCGCAGGCTACGTCGTCCA 1620
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Db   1561 TCATCACTTGCCGCTGGCGTGGTTTGGGTGAGTGGATTGCCCGCAGGCTACGTCGTCCA 1620
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Qy   1621 CCACGCTTCAACCCATACCGTGCATTACCAAGGCGAATGAGTTCTCCTTCCAGGAGGAA 1680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1621 CCACGCTTCAACCCATACCGTGCATTACCAAGGCGAATGAGTTCTCCTTCCAGGAGGAA 1680
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Qy   1681 GCTGAGCAGAATCAGCGCCGCGGCCAGCAGAGAAAAACGTCCAAAGACTAATCAGAGATTCGGTAAT 1740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1681 GCTGAGCAGAATCAGCGCCGCGGCCAGCAGAGAAAAACGTCCAAAGACTAATCAGAGATTCGGTAAT 1740
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Qy   1741 AAAAGGTAAAAATCAACCTGCTTAGGCGTCTTTCGCTTAAAATAGCGTAGAATATCGGGTC 1800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1741 AAAAGGTAAAAATCAACCTGCTTAGGCGTCTTTCGCTTAAAATAGCGTAGAATATCGGGTC 1800
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Qy   1801 GATCGCTTTAAACACTCAGGAGGATCCTTGCCGCGCCAAAATCACGGACACTCGTCCCAC 1860
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1801 GATCGCTTTAAACACTCAGGAGGATCCTTGCCGCGCCAAAATCACGGACACTCGTCCCAC 1860
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Qy   1861 CCCAGAATCCCTTCACGCTGTTGAAGAGGAAACCGAGCCGCGGGTACCG 1909
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Db   1861 CCCAGAATCCCTTCACGCTGTTGAAGAGGAAACCGAGCCGCGGGTACCG 1909
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RESULT 2
US-09-431-099-1
; Sequence 1, Application US/0943109
; Patent No. 6410705
; GENERAL INFORMATION:
; APPLICANT: Degussa-HOls AG
; APPLICANT: Forschungszentrum-JOlich GmbH
; TITLE OF INVENTION: New nucleotide sequences coding for the thrE gene and process fo
; TITLE OF INVENTION: enzymatic production of L-threonine with coryneform bacteria.
; FILE REFERENCE: 990079 BT
; CURRENT APPLICATION NUMBER: US/09/431,099
; CURRENT FILING DATE: 1999-11-01
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 2817
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum ATCC14752
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (398)..(1864)
; OTHER INFORMATION: thrE-Gen
US-09-431-099-1

Query Match   96.2%;   Score 1836.6;   DB 4;   Length 2817;
Best Local Similarity   99.0%;   Pred. No. 0;
Matches 1848;   Conservative   0;   Mismatches   19;   Indels   0;   Gaps   0;

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Qy     38 CCCCTTTGACCTGGTTGTTATTGAGCTGGAGAAGAGACTTGAACTCTCAACCTACGCATTA 97
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    156 CCCCTTTGACCTGGTTGTTATTGAGCTGGAGAAGAGACTTGAACTCTCAACCTACGCATTA 215
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Qy     98 CAAGTGGTTGGCTGCAATTGCGCCACTCCAGCACCCGAGATGCTGATGATCAACAAC 157
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    216 CAAGTGGTTGGCTGCAATTGCGCCACTCCAGCACCCGAGATGCTGATGATCAACAAC 275
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Qy    158 TACGAATACGTATCTTAGCTGTATGTGCTATGTGTACATCACAATGGAATTCGGGCTAGTATCTG 217
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    276 TACGAATACGTATCTTAGCTGTATGTGCTATGTGTACATCACAATGGAATTCGGGCTAGTATCTG 335
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us-09-963-521-3.rnl

Right column:

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Qy  1298  TTACTGCGCTGATGGGTTCGCGTTTCATTACCTTCGTTGTTATTTAGGCCCGTCT  1357
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Db  1416  TTACTGCGCTGATGGGTTCGCGTTTCATTATTACCTTCGTTGTTATTTAGGCCCGTCT  1475

Qy  1358  CTGCCGCTGCGATTGCTGCAACAGCAGTGGTTTCACTCGCGTGGTTGCTTGCCCGTCGAT  1417
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1476  CTGCCGCTGCGATTGCTGCAACAGCAGTGGTTTCACTCGCGTGGTTGCTTGCCCGTCGAT  1535

Qy  1418  TCTTGATTCCACCGTTGATGTGTGGCGATTGCCGGCATCACCACCAATGCTTCCAGGTCTAG  1477
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1536  TCTTGATTCCACCGTTGATGTGTGGCGATTGCCGGCATCACCACCAATGCTTCCAGGTCTAG  1595

Qy  1478  CAATTACCGCGGAATGTACGCCACCCTGAATGATCAAACACTCATGGGTTTCACCAACA  1537
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Db  1596  CAATTACCGCGGAATGTACGCCACCCTGAATGATCAAACACTCATGGGTTTCACCAACA  1655

Qy  1538  TTGCGGTTGCTTTAGCCACTGCTTCATCACTTGCCGCTGCGTGGTGTTTGGGTGAGTGGA  1597
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Db  1656  TTGCGGTTGCTTTAGCCACTGCTTCATCACTTGCCGCTGCGTGGTGTTTGGGTGAGTGGA  1715

Qy  1598  TTGCCCGCAGGCTACGTCGTTCCACCACGCGCTTCAACCCATACCGTGCATTTACCAAGGCGA  1657
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1716  TTGCCCGCAGGCTACGTCGTTCCACCACGCGCTTCAACCCATACCGTGCATTTACCAAGGCGA  1775

Qy  1658  ATGAGTTCCTTCCAGGAGGAAGCTGAGCAGAATCAGCGCCGCAGAGAAAACGTCCAA  1717
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1776  ATGAGTTCCTTCCAGGAGGAAGCTGAGCAGAATCAGCGCCGCAGAGAAAACGTCCAA  1835

Qy  1718  AGACTAATCAGAGATTCGTAATAAAGGTAAAAATCAACCTGCTTTAGGCGTCTTTCGCT  1777
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Db  1836  AGACTAATCAAAGATTCGGTAATAAAGGTAAAAATCAACCTGCTTTAGGCGTCTTTCGCT  1895

Qy  1778  TAAATAGGCTAGAATATCGGGTCGATCGCTTTAAACACTCAGGAGGATCCTTGCCGCGCC  1837
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Db  1896  TAAATAGGCTAGAATATCGGGTCGATCGCTTTAAACACTCAGGAGGATCCTTGCCGCGCC  1955

Qy  1838  AAAATACCGGACACTCGTCTCCACCCCAGAATCCTTCACGCTGTTGAAGAGGAAACCGCA  1897
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Db  1956  AAAATACCGGACACTCGTCTCCACCCCAGAATCCCTTCACGCTGTTGAAGAGGAAACCGCA  2015

Qy  1898  GCCGGGGG  1904
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Db  2016  GCCGGTG  2022
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RESULT 3
US-09-602-787A-557
; Sequence 557, Application US/09602787A
; Patent No. 6965561
; GENERAL INFORMATION:
;   APPLICANT: Pompejus, Mark
;   APPLICANT: Kr"ger, Burkhard
;   APPLICANT: Sch"der, Hartwig
;   APPLICANT: Zelder, Oskar
;   APPLICANT: Haberhauer, Gregor
;   TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS
;   TITLE OF INVENTION: INVOLVED IN MEMBRANE SYNTHESIS AND MEMBRANE
;   TITLE OF INVENTION: TRANSPORT
;   FILE REFERENCE: BGI-125CP
;   CURRENT APPLICATION NUMBER: US/09/602,787A
;   CURRENT FILING DATE: 2000-06-23
;   PRIOR APPLICATION NUMBER: USSN 60/141031
;   PRIOR FILING DATE: 1999-06-25
;   PRIOR APPLICATION NUMBER: DE 19931454.3
;   PRIOR FILING DATE: 1999-07-08
;   PRIOR APPLICATION NUMBER: DE 19931478.0
;   PRIOR FILING DATE: 1999-07-08
;   PRIOR APPLICATION NUMBER: DE 19931563.9
;   PRIOR FILING DATE: 1999-07-08
;   PRIOR APPLICATION NUMBER: DE 19932122.1
;   PRIOR FILING DATE: 1999-07-09
;   PRIOR APPLICATION NUMBER: DE 19932124.8
;   PRIOR FILING DATE: 1999-07-09

Left column:

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Qy  218   GTGAACCGTGCATAAACGACCTGTGATTGGACTCTTTTTCCTTGCAAAATGTTTTCCAGC  277
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Db  336   GTGAACCGTGCATAAACGACCTGTGATTGGACTCTTTTTCCTTGCAAAATGTTTTCCAGC  395

Qy  278   GGATGTTGAGTTTGCGACCCTCGTGCCGCATTCAACAGTTGACGCTGCAAAAGCCG  337
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  396   GGATGTTGAGTTTGCGACCCTCGTGCCGCATTCAACAGTTGACGCTGCAAAAGCCG  455

Qy  338   CACCTCCGCCATCGCCACTAGCCCGATTGATCTCACTGACCATAGTCAAGTGGCCGGTG  397
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  456   CACCTCCGCCATCGCCACTAGCCCGATTGATCTCACTGACCATAGTCAAGTGGCCGGTG  515

Qy  398   TGATGAATTGGCTGCGGAGAATTGGCGATATTTGCTTTCTTCAGGTACGTCAAATAGTG  457
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Db  516   TGATGAATTGGCTGCGGAGAATTGGCGATATTTGCTTTCTTCAGGTACGTCAAACAGTG  575

Qy  458   ACACCAAGGTACAAGTTCGAGCAGTGACCTCTGCGTACGGTTTGTACTACACGCACGTGG  517
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Db  576   ATACCAAGGTGCAAGTTCGAGCAGCGGTGACCTCGTATGGCCTGTACTATACGCATGTGG  635

Qy  518   ATATCACGTTGAATACGATCACCATCTTCACCAACATCGGTGTGGAGAGGAAGATGCCGG  577
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  636   ATATCACGTTGAATACGATCACCATCTTCACCAACATCGGTGTGGAGAGGAAGATGCCGG  695

Qy  578   TCAACGTGTTTCATGTTGTGGCAAGTTGGACACCAACTTCTCCAAACTGTCTGAGGTTG  637
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Db  696   TCAACGTGTTTCATGTTGTGGCAAGTTGGACACCAACTTCTCCAAACTGTCTGAGGTTG  755

Qy  638   ACCGGTTTGATCCGTTCCATTCAGGCTGGCGCACCCCGCCTGAGGTTGCCGAGAAAATCC  697
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  756   ACCGGTTTGATCCGTTCCATTCAGGCTGGCGTGCTGCTACCCCGCCTGAGGTTGCCGAGAAAATTC  815

Qy  698   TGGACGAGTTGGAGCAATCCCCTGCGTCTTATGGTTCCCTGTTGCTTGGCTGGG  757
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  816   TGGACGAGTTGGAGCAATCGCCTGCGTCTTATGGTTCCCTGTTGCTTGGCTGGG  875

Qy  758   CAATGATGGGTGGTGCTGTGTTTGGCTGGTGGTGTGGGATGGCAGTTTCCCTAATTG  817
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  876   CAATGATGGGTGGTGCTGTGTTTGGCTGGTGGTGTGGGATGGCAGTTTCCCTAATTG  935

Qy  818   CTTTTATTACCGCGTTCACGACGATCATTGCCACGACGTCATTTTGGGAAAGAAGGGTTTGC  877
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  936   CTTTTATTACCGCGTTCACGACGATCATTGCCACGACGTCATTTTGGGAAAGAAGGGTTTGC  995

Qy  878   CTACTTTCTTCCAAAATGTGTTGGTGGTGGTTTATTGCCACGCTGCCTGCACGCGATTGCTT  937
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Db  996   CTACTTTCTTCCAAAATGTGTTGGTGGTGGTTTATTGCCACGCTGCCTGCACGCGATTGCTT  1055

Qy  938   ATTCTTTGGCGTTGCAATTTGGTCTTGAGATCAAAACCGAGCCAGATCATCGCATCTCGGAA  997
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Db  1056  ATTCTTTGGCGTTGCAATTTGGTCTTGAGATCAAAACCGAGCCAGATCATCGCATCTCGGAA  1115

Qy  998   TTGTTGTGTCTGTTGGCAGGTTTGGCAGGTTTGACACACTCGTGCAATCTCTGCAGGACGCATCACGGGCG  1057
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Db  1116  TTGTTGTGTCTGTTGGCAGGTTTGGCAGGTTTGACACACTCGTGCAATCTCTGCAGGACGCATCACGGGCG  1175

Qy  1058  CTCCGGTGACAGCAAGTGCACGATTTTCGAAACACTCCGTTACCGGCGCCATTGTTG  1117
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1176  CTCCGGTGACAGCAAGTGCACGATTTTTGAAACACTCCGTTACCGGCGCCATTGTTG  1235

Qy  1118  CTGGCGTGGGGTTTGGGCATTCAGCTTTCTGAAATCTTCATGTCATGTTGCCTGCCATGG  1177
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1236  CTGGCGTGGGGTTTGGGCATTCAGCTTTCTGAAATCTTCATGTTGCATGTCATGTTGCCTGCCATGG  1295

Qy  1178  AGTCCGCTGCAGCACCTAATTATTCGTCTACATTCGCCCGCCATTATCGCTGCTGGCGTCA  1237
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy  1238  CCGCAGCGGCCTTCGCAGTGGGTTGTTACGCCGAGTGGTCCTCGGTGATTATTGCGGGGC  1297
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; PRIOR APPLICATION NUMBER: DE 19932125.6
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932128.0
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932180.9
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932182.5
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932190.6
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932191.4
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932209.0
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932212.0
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932227.9
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932228.7
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932229.5
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932230.9
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932927.3
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19933005.0
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: DE 19933006.9
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: DE 19940764.9
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: DE 19940765.7
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: DE 19940766.5
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: DE 19940830.0
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: DE 19940831.9
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: DE 19940832.7
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: DE 19940833.5
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: DE 19941378.9
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: DE 19941379.7
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: DE 19942077.7
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: DE 19942078.5
; PRIOR FILING DATE: 1999-09-03
; PRIOR APPLICATION NUMBER: DE 19942079.3
; PRIOR FILING DATE: 1999-09-03
; PRIOR APPLICATION NUMBER: DE 19942088.2
; PRIOR FILING DATE: 1999-09-03
; NUMBER OF SEQ ID NOS: 678
SEQ ID NO 557
; LENGTH: 1590
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (101)..(1567)
; OTHER INFORMATION: RXN00349
US-09-602-787A-557

Query Match        83.3%;  Score 1590;  DB 4;  Length 1590;
Best Local Similarity  100.0%;  Pred. No. 0;
Matches 1590;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;
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Qy   180 TGTGTACATCACAATGGAATTCGGGGCTAGAGTATCTGTGAACCGTCGTCATAAACGACCT 239
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Db     1 TGTGTACATCACAATGGAATTCGGGGCTAGAGTATCTGTGAACCGTCGTCATAAACGACCT 60

Qy   240 GTGATTGGACTCTTTTCCTTGCAAAATGTTTCCAGCGGATGTTGAGTTTGCGACCCT 299
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61 GTGATTGGACTCTTTTCCTTGCAAAATGTTTCCAGCGGATGTTGAGTTTGCGACCCT 120

Qy   300 TCGTGGCCGCATTCAACAGTTGACGCTGCAAAAGCGCCACCTCCGCCACTCGCCACTAGC 359
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 TCGTGGCCGCATTCAACAGTTGACGCTGCAAAAGCGCCACCTCCGCCACTCGCCACTAGC 180

Qy   360 CCCGATTGATCTCACTGACCATATGCAAGTGGCCGGTGTGATGAATTGGCTGCGAGAAT 419
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 CCCGATTGATCTCACTGACCATATGCAAGTGGCCGGTGTGATGAATTGGCTGCGAGAAT 240

Qy   420 TGGCGGATATTTGCTTTCTTCAGTACGTCAAATAGTGACACCAAGGTACAAGTTCGAGC 479
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 TGGCGGATATTTGCTTTCTTCAGTACGTCAAATAGTGACACCAAGGTACAAGTTCGAGC 300

Qy   480 AGTGACCTCTGCGTACGGTTTGTACTACACGCACGTGGATATCACGTTGAATACGATCAC 539
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 AGTGACCTCTGCGTACGGTTTGTACTACACGCACGTGGATATCACGTTGAATACGATCAC 360

Qy   540 CATCTTCACCAACATCCGTGTGGAGAGGAAGATGCCGGTCAACGTGTTCATGTTGTAGG 599
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 CATCTTCACCAACATCCGTGTGGAGAGGAAGATGCCGGTCAACGTGTTCATGTTGTAGG 420

Qy   600 CAAGTTGGACACCAACTTCTCCAAACTGTCTGAGGTTGCCGAGAAAATCCTGGCAATCCCC 659
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 CAAGTTGGACACCAACTTCTCCAAACTGTCTGAGGTTGCCGAGAAAATCCTGGCAATCCCC 480

Qy   660 GGCTGGTGCGACCCCGCCGCTGAGTTGCCGACGAGTTGGAGCAATCCCC 719
             |||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 GGCTGGTGCGACCCCGCCGCTGAGTTGCCGACGAGTTGGAGCAATCCCC 540

Qy   720 TGCGTCTTATGGTTTCCGTGTTGCGTTGCTTGGCTGGCAATGATGGGTGGTGCTGTTGC 779
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541 TGCGTCTTATGGTTTCCGTGTTGCGTTGCTTGGCTGGCAATGATGGGTGGTGCTGTTGC 600

Qy   780 TGTGCGTTGGGTGGTGGGATGGCAGTTTCCCTAATTGCTTTTATTACCGCGTTCACGAT 839
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601 TGTGCGTTGGGTGGTGGGATGGCAGTTTCCCTAATTGCTTTTATTACCGCGTTCACGAT 660

Qy   840 CATTGCCACGACGTCATTTTTGGGAAAAGAAGGGTTTGCCTACTTTCTTCCAAAATGTTGT 899
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   661 CATTGCCACGACGTCATTTTTGGGAAAAGAAGGGTTTGCCTACTTTCTTCCAAAATGTTGT 720

Qy   900 TGGTGGTTTTATTGCCACGCTGCCTCGACGTCGATTGCTTATTCTTTGGCGTTGCAATTTGG 959
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   721 TGGTGGTTTTATTGCCACGCTGCCTCGACGTCGATTGCTTATTCTTTGGCGTTGCAATTTGG 780

Qy   960 TCTTGAGATCAAACCGGAGCCAGATCATCGCATCTGAATTCTGTGTGTCGTTGGCAGGTTT 1019
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   781 TCTTGAGATCAAACCGGAGCCAGATCATCGCATCTGAATTCTGTGTGTCGTTGGCAGGTTT 840

Qy  1020 GACACTCGTCAATCTCGAGGACGACGGCATCACGGGCGCTCCGGTCGACGACAGTGCACG 1079
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   841 GACACTCGTCAATCTCGAGGACGACGGCATCACGGGCGCTCCGGTCGACGACAGTGCACG 900

Qy  1080 ATTTTTCGAAACACTCCGTTTACCGGCGATTGTTGCTCGGCGTGGGTTTGGGCATTCA 1139
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   901 ATTTTTCGAAACACTCCGTTTACCGGCGATTGTTGCTCGGCGTGGGTTTGGGCATTCA 960

Qy  1140 GCTTTCTGAAATCTTGCATGTCATGTGCCATGAGTCCGCTGCAGCCACCTAATTA 1199
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   961 GCTTTCTGAAATCTTGCATGTCATGTGCCATGAGTCCGCTGCAGCCACCTAATTA 1020

Qy  1200 TTCGTCTACATTCGCCCGCCATTATCGCTGGCGTGGTGGCCTTCGCAGTCGTGGG 1259
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1021 TTCGTCTACATTCGCCCGCCATTATCGCTGGCGTGGTGGCCTTCGCAGTCGTGGG 1080

Qy  1260 TTGTTACGCGGAGTGTCCTCGGTGATTATTGCGGGGCTTACTGCCTGATGGGTTCTGC 1319
```

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Qy    651  TTCCATTCAGGCTGGTGGTGCGACCCGCCTGAGGTTGCCGAGAAATCCTGGCGGTTGCCGAGACGAGTTGGA  710
            ||||||||||||||||||||||| |||||||||||||||| ||||  | ||||||||||||||||||||||
Db 4180333  GCGGATAACCTCCGTGGCGTCGCAGTCGACTCACGAGGCTATGCGGCTGGGCAATGATGATGGGTGG  4180392

Qy    711  GCAATCCCCTGGCCCACCCCTACCCGCTGCGCCGCCTGCCGCCGCGCGGGGGCGGGGCCTTCGCACT  770
            |  ||||||||||  ||| |||||||||||||||||||||||||||||||||||||||||||||
Db 4180393  CGAACGGCGCTGGTGCTGCTGGCGCCGCCTGTTCCCGACGTTCCCTAATTGCTTTATTACCGC  4180452

Qy    771  TGCTGTTGCGTGCGTGGTTGCTTGCTTCGTCGGCGGGATGGCAGGTTCCCGGCTGCCGGTCTCGGTCTCG  830
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4180453  CGGGCTCGCCATGTTGCTCGGCGAACCTGGCTGACCTGGTCTCGGCGGAATGTACGGAATGTACGTC  4180512

Qy    831  GTTCACGATCATTGCCACGACGTCATTTTTGGGAAAGAGAGGGTTTGCCTACTTTTCTTCCA  890
            ||||||||||||||||||||||||||||||||||||  || ||||||||||||||||||||
Db 4180513  TGGCGTGATCGACCGAACTGGGCCGCCGCTGCTCGCATCGATTGCTTTAATCTTTTGGCGTT  4180572

Qy    891  AAATGTTGTGTGGTTTATTGCGCAGGCTGCGTCATCGATTGTCGGTTGCTGTTTTAGCCACTGC  950
            |||||||||||||||||||| |||||||||||||||||  ||||||||||||||||||||||
Db 4180573  GCGCGTGTTCGGCGGGGATCGGACCCTGGTCGCGGCTTCGCTCGGAATTGTTGTCGTGTT  4180632

Qy    951  GCAATTTGGTCTTGAGATCAAACGAGCCAGATCAATCGAGTGGGCCACCGGAATCGTTGTCTGCTGCT  1010
            ||                          ||||||||||||||||||||||||||||||||||||
Db 4180633  CCA                         GGATCCGACCGCGCTGGTGGCCACCGGAATCGTTGTGTCTGCT  4180677

Qy   1011  GGCAGGTTTGACACTCGTGCAATCTCGAGGACGGCATCACGGGCGCCTCCGGTCGACAGC  1070
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4180678  GTCTGGGATGACCTTGGTCGGGTTCGATGCGAGGACGCGGTCACCCGGTACAATGCCCGC  4180737

Qy   1071  AAGTGCACGACATTTTCGAAACACACTCCTGTTTTACCGGCGCCAGGATCGTCGTCGTGGCGT-----  1124
            |||||||                ||||| ||||||||||||||||||||||||||||||
Db 4180738  ACTCGCCCGGCTTGGCGACGCCCTGTTCCTGACCGTGAAATCTTGCATGTCATGTCGGCATCCTCAT  4180797

Qy   1125  ----------GGGGTTGGCATTCAGCTTTCTGAAATCGCATCCAGATGCCGGGCGTCAGCCGGCGCAACCAC  1175
                      |||||||||||||||||||||||||||||| |||||||||||||||||||||||||||
Db 4180798  CTCGTTGCGGGGGCGCTCACCAATGCCGGGCGTCATCATCTTGCTCTACATTCGCCCGCATTATCGCTGGTTGGCGT  4180857

Qy   1176  GGAGTCCGCTGCAGCACCTAATTATTCGTCTCACATTCGCCCGCATTATCGTCTGGTTGGCGCT  1235
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4180858  GACGCTCGCCACCCCGGCATGCCGATTCTCGTTCGCGGTAAGCCGGTGCGGGCGCT  4180917

Qy   1236  CACCGCCAGCGGCCTTCGCAGTCGAGTGGTTGTTACGCGGAGTGGTGCTCCTCCGGAGTCGTGCTGATTATTCGGG  1295
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||
Db 4180918  GTCCGGGCGTGTGCTGACGATCGGCAGATCGGCCAGCTATGCGCCGTACGTTCTGTGCCACCGGCACACCCGG  4180977

Qy   1296  GCTTACTGC---GCTGATGGGTTCGCTGGTTTTATTACCTTCGTTGTTGTTGTTATTAGGCCC  1352
            ||||| || |||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4180978  ACTTCTCCGGCCGGACTTCGCGGGTTGTGCTCATCGACTCGGCGGCGCGGGGTTCGCCG  4181037

Qy   1353  CGTCTCTGCCGCGTCGCATTGCTGCGAACAGCAGTTGGTTTCACTGGTGTTTGCTTGTCCCG  1412
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4181038  AGTGGTCGCCGCCACCTGGACCGGCGCCGCGGATCGGACTTCTTGGCCACCCCTGATCTCAAT  4181097

Qy   1413  TCGATTCTTGATTCCACCGTTGATTGTGCGGATTGGCGATTGCCGGCATCACCAATGCTTCCAGG  1472
            |||||||||||||||||||||||||| ||||||||||||||||||||||| ||||| ||||||
Db 4181098  CCGTTCGGCAGGCTTCCCGGCCTTGTCGTGGTGACGGCCACCGGCATGCCCGATGCGCCGGGG  4181157

Qy   1473  TCTAGCAATTTACCGGCGGAATGTACGC---CACCCTGAATGATCAAACACTCATGGGTTT  1529
            ||||||||||||||||||||||||||||   |||||||||||||||||||||||||||||
Db 4181158  CCTTTGCGGTCTTCGCGGTCGTTCGCGTTTCGCCGTCAATCAATGACACACCCGACGCGGTCT  4181217

Qy   1530  CACCAAACATTGCCGGTTGCTTTAGCCACTCACTTGCCGCTGCCGTGGTGGTTTTGGG  1589
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4181218  GACCCCAGCTGCTCGGAAGCGCCGACTGCACTCGCGCTTGGCAGCGCGGTGGTTGTTGGG  4181277

Qy   1590  TGAGTGGATTGCC  1602
            ||||||||||||
Db 4181278  CGAGTTCCTCGCC  4181290
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RESULT 5
US-09-103-840A-1
; Sequence 1, Application US/09103840A

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Db   1081  TTGTTACGCGGAGTGGTGCTCCTCCGGTGATTATTCGGGAGGCCCGTCTCGCCGCTGCGCCGCTGATGGGTTCTGC  1140
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1320  GTTTTATTACCTTCGTTGTTGTTGTTATTAGGCCCGTCTCGCCGCTGCGCCGCTGATGGGTTCTGCGCAAC  1379

Db   1141  GTTTTATTACCTTCGTTGTTGTTGTTATTAGGCCCGTCTCGCCGCTGCGCCGCTGATGGGTTCTGCGCAAC  1200
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1380  AGCAGTTGGTTCACTGGTGTTGCTTGCTTCGTCCGTCGATTCTTGATTCCACCGGTTGATTGT  1439

Db   1201  AGCAGTTGGTTCACTGGTGTTGCTTGCTTCGTCCGTCGATTCTTGATTCCACCGGTTGATTGT  1260
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1440  GGCGATTGCCGGCATCACCACCAATGCTTCCAGGTCTCAGCAATTTACCGGCGTCTAGCAGC  1499

Db   1261  GGCGATTGCCGGCATCACCACCAATGCTTCCAGGTCTCAGCAATTTACCGGCGAATGTACGC  1320
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1500  CACCCTGAATGATCAAACACTCATGGGTTTCACCGGTTTCACCCGTTGCTTTAGCCACTGC  1559

Db   1321  CACCCTGAATGATCAAACACTCATGGGTTTCACCGGTTTCACCCGTTGCTTTAGCCACTGC  1380
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1560  TTCATCACTTGCCGCTGCCGTGGTTGGGTAGTGAGTTGCCCGCAGGCTACGTCGTCC  1619

Db   1381  TTCATCACTTGCCGCTGCCGTGGTTGGGTAGTGAGTTGCCCGCAGGCTACGTCGTCC  1440
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1620  ACCACGCTTCAACCCATACCGTGCATTTACCAAGAGGCGAATGAGTTCTCCTTCCAGGAGGA  1679

Db   1441  ACCACGCTTCAACCCATACCGTGCATTTACCAAGAGGCGAATGAGTTCTCCTTCCAGGAGGA  1500
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1680  AGCTGAGCAGAATCAGCGCCGCAGAGAAAACGCTCAAAGACTAATCAGAGATTCGGTAA  1739

Db   1501  AGCTGAGCAGAATCAGCGCCGCAGAGAAAACGCTCAAAGACTAATCAGAGATTCGGTAA  1560
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1740  TAAAAGGTAAAAAATCAACCTGCTTAGGCGT  1769

Db   1561  TAAAAGGTAAAAAATCAACCTGCTTAGGCGT  1590
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RESULT 4
US-09-103-840A-2
; Sequence 2, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
;   APPLICANT: FLEISCHMAN, Robert D.
;   APPLICANT: WHITE, Owen R.
;   APPLICANT: FRASER, Claire M.
;   APPLICANT: VENTER, John C.
;   TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
;   TITLE OF INVENTION: TUBERCULOSIS
;   FILE REFERENCE: 24366-20007.00
;   CURRENT APPLICATION NUMBER: US/09/103,840A
;   CURRENT FILING DATE: 1998-06-24
;   NUMBER OF SEQ ID NOS: 2
;   SOFTWARE: PatentIn Ver. 2.1
US-09-103-840A-2
;   SEQ ID NO 2
;   LENGTH: 4403765
;   TYPE: DNA
;   ORGANISM: Mycobacterium tuberculosis
;   FEATURE:
;   OTHER INFORMATION: CDC 1551
;   OTHER INFORMATION: "n" bases at various positions throughout the sequence
;   OTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2

Query Match           4.5%;   Score 86.6;  DB 3;  Length 4403765;
Best Local Similarity 45.6%;  Pred. No. 1.3e-14;
Matches  498;  Conservative  0;  Mismatches 559;  Indels 36;  Gaps  4;
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Qy    531  TACGGTCCGGCAAGTTGGACACCAACTTCTCCAAACTGTCTGAGGTTGACCGGTTGACGGTTCA  590
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4180213  TACCACCATCATCGTTCGCCGCCGCTAGCGACCCACCAGCAGACTCACCTCCGGGTCCGTCGTTCGGTCACCATCATGCG  4180272

Qy    591  TGTTGTTAGGCAAGTGGACACCAACTGTTCTCCAAACTGTCTGAGGTTGACCGGTTGATCCG  650
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4180273  GTCGGGTCCGGACGACCCGGTCCACTGGACTGACCGGCCTGCCGCCGAACTGCGATCAGCTCGTTCA  4180332
```

```
; Patent No. 6294328
; GENERAL INFORMATION:
;   APPLICANT: FLEISCHMAN, Robert D.
;   APPLICANT: WHITE, Owen R.
;   APPLICANT: FRASER, Claire M.
;   APPLICANT: VENTER, John C.
;   TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
;   TITLE OF INVENTION: TUBERCULOSIS
;   FILE REFERENCE: 24366-20007.00
;   CURRENT APPLICATION NUMBER: US/09/103,840A
;   CURRENT FILING DATE: 1998-06-24
;   NUMBER OF SEQ ID NOS: 2
;   SOFTWARE: PatentIn Ver. 2.1
;
; SEQ ID NO 1
;   LENGTH: 4411529
;   TYPE: DNA
;   ORGANISM: Mycobacterium tuberculosis
;   OTHER INFORMATION: H37Rv
US-09-103-840A-1

Query Match            4.5%;    Score 86.6;  DB 3;  Length 4411529;
Best Local Similarity 45.6%;    Pred. No. 1.3e-14;
Matches   498;  Conservative    0;  Mismatches 559;  Indels   36;  Gaps   4;

Qy     531 TACGATCACCATCTTCACCAACATCGGTGTGGAGGAAGATCCGGTCAACGTGTTCA 590
           |||||| ||||| ||   ||  |||   ||    |||  ||| |||
Db 4187965 TACCACCATCATCGTCGTCCGCGTAGCGACCACAGACACTCCGCCGGTCACCATCATGCG 4188024

Qy     591 TGTTGTAGGCAAGTTGACACCAACTTCTCCAAACTGTCTGAGGTTGACCGTTTGATCCG 650
           ||||||
Db 4188025 GTCGGGTCCGGACACCGGTCGGTGCGACCCGCCTGAGGTTGCCGAGAGTTGGA 4188084

Qy     651 TTCCATTCAGGCTGGTGCGACCCGGTCGAGTGCGTCGCAGTTGCCAAGGAGAGTTGGA 710
           ||||||||
Db 4188085 GCGGATAACCTCCGGTGGCGTGCAGTCGACCAGGCTCACGAGGCTATGGACGAGTTGAC 4188144

Qy     711 GCAATCCCCTGCGCTCTTATGGTTCCCTGTTGCGTTGGCTGGGCAATGATGGGTGG 770
           ||   |||   |||
Db 4188145 CGAACGGCCCCACCCTACCCGGCTCGCGACCCGCGGGGGCGGCGCTTCGCACT 4188204

Qy     771 TGCTGTTGCTGTCGTTGGGGTGGTGATGGCAGGTTTCCCTAATTGCTTTATTACCGC 830
           ||   ||||||
Db 4188205 CGGCCGTCGCCATGTTGCTCGGCGGAACCTGGCTGACCTGCGCTTGGCGCCGTGACGTC 4188264

Qy     831 GTTCACGATCATTGCCACGACGACTCATTTTGGGAAAGAAGGGTTTGCCTACTTCTTCCA 890
           ||
Db 4188265 TGGCGTGATCGACCGACTGGGCCGGCTGCTCAACCGGATCGGGACCCCGTTGTTCTTCCA 4188324

Qy     891 AAATGTTGTTGGTGGGTGTTTATTGCCACGCTGCCTGCATCGATTGCTTATTCTTTGGCGTT 950
           ||   |||||
Db 4188325 GCGCGGTGTTCGGCGCGGGGATCGGACCCCTGTCTGCGTCGGCGGCCTTACCTGATCGCCGG 4188384

Qy     951 GCAATTTGGTCTTGAGATCAAACCAGCCAGATCATCGCATCTGGAATTGTTGTGCTGTT 1010
           |||
Db 4188385 GGATCCGACCACCGGCCTGGTCGTGCCACCGGAATCGTTGTTGTGCTGCT 4188429

Qy    1011 GGCAGGTTTGACACTCGTGCAATCTGCAGAGCAGGCGGCATCACGGCGCTCCGGTGACAGC 1070
           |||
Db 4188430 GTCTGGGATGCAGCCTTCGTGTGGTTCATTTATTGTCCACGCTGCAATGCTCACCGC 4188489

Qy    1071 AAGTGCACGATTTTTCGAAACACTCCTGTTACCGGCGGCATTGTTGCTCGGCGT----- 1124
           |||
Db 4188490 ACTCCGCCCGGCTTGGGCAGCGGCGATCGGTCGCGGCAGGATCGTCGTCGGCATCCTCAT 4188549

Qy    1125 --------GGGTTTGGGCATTCAGCTTTCTGAAATCTTGCATGTCATGTTGCCTGCCAT 1175
                   |||
Db 4188550 CTCGTTGCGGGGGCGTCAGCAGCACGTTGCCGCCGCCATTATCGCCTGGTGGCGT 4188609

Qy    1176 GGAGTGCCGCTGCAGCACCTAATTATTCGTCTACATTCGCCGCCATTATCGCCTGGTGGCGT 1235
           |||
Db 4188610 GACGCGCTCGCACCACCCGGGCATGCCCGTACCGGTCGTGCGCGTGAAGCCGGTGCGCGCGCT 4188669

Qy    1236 CACCGCAGCCGGCCGCCTTCGCAGTGGCGTGTTACGCGGAGTGGTCCTCGGTGATTATTGCGGG 1295
           |||
Db 4188670 GTTCGGCGGCGTGTGCGTCCTGCTCGCATCGCTGTGCCGCTACGGTTCGTGGTCACGCGCCG 4188729

Qy    1296 GCTTACTGC---GCTGATGGGGTTCTTCGCGTTTTATTACCCTCTTCGTCGTGTTATTAGGCCC 1352
           ||
Db 4188730 ACTCTCGGCCGGACTCGGCGAACTGGTGCTCATCGGAACTGGTGGTTTGTGGTTTCGGCCG 4188789

Qy    1353 CGTCTCTGCCGCTGCGATTGCTGCAACAGCAGTGGTTCACTGGTGTTTGCTGCCG 1412
           ||
Db 4188790 AGTGGTCGCCACTGGCCACCGGCACCGGCGATCGGCGGCTCCTTGGCCACCCTGATCTCAAT 4188849

Qy    1413 TCGATTCTTGATTCCACCGTTGATTGTGGCGATTGCCGGCATCACACCCAAATGCTTCAGG 1472
           |||
Db 4188850 CCGTCGGCGAGGCTCCCGCCTTGGTGACGGCCACCGGCCATCATGCCGATGCTGCCGGG 4188909

Qy    1473 TCTAGCAATTTACCGCCGGAATGTACGC---CACCCTGATGATCAAACACTCATGGGGTTT 1529
           ||
Db 4188910 CCTTGCCGTCTTCCGTGCCGTGTTCGGCGTTCGGCGGCCTTGGCAGCCGGGGTGTGTTGGG 4188969

Qy    1530 CACCAACATTGCGGTTGCTTTAGCCACTGCTTCATCACTTGCCGCTGCCGGTGGTTTGGG 1589
           |||
Db 4188970 GACCCAGCTGCTGGAAGCGGCCGCGACTGACTGCACGCGCCACCGCTTGGCAGCCGGGCTGG 4189042

Qy    1590 TGAGTGGATTGCC 1602
           |||
Db 4189030 CGAGTTCCTCGCC 4189042
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RESULT 6
US-08-232-463-14

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; Sequence 14, Application US/08232463
; Patent No. 5670367
; GENERAL INFORMATION:
;   APPLICANT: DORNER, F.
;   APPLICANT: SCHEIFLINGER, F.
;   APPLICANT: FALKNER, F. G.
;   TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
;   NUMBER OF SEQUENCES: 52
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: Foley & Lardner
;     STREET: 1800 Diagonal Road, Suite 500
;     CITY: Alexandria
;     STATE: VA
;     COUNTRY: USA
;     ZIP: 22313-0299
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Floppy disk
;     COMPUTER: IBM PC compatible
;     OPERATING SYSTEM: PC-DOS/MS-DOS
;     SOFTWARE: PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/08/232,463
;     FILING DATE:
;     CLASSIFICATION: 435
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: US/07/935,313
;     FILING DATE:
;     APPLICATION NUMBER: EP 91 114 300.6
;     FILING DATE: 26-AUG-1991
;   ATTORNEY/AGENT INFORMATION:
;     NAME: BENT, Stephen A.
;     REGISTRATION NUMBER: 29,768
;     REFERENCE/DOCKET NUMBER: 30472/114 IMMU
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: (703)836-9300
;     TELEFAX: (703)683-4109
;     TELEX: 899149
; INFORMATION FOR SEQ ID NO: 14:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 7218 base pairs
;     TYPE: nucleic acid
;     STRANDEDNESS: single
;     TOPOLOGY: linear
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;   IMMEDIATE SOURCE:
;     CLONE: pTzgpt-F1s
; US-08-232-463-14

Query Match        2.5%;  Score 47.6; DB 1;  Length 7218;
Best Local Similarity   3.6%;  Pred. No. 0.00059;
Matches  14;  Conservative  218;  Mismatches 162;  Indels   0;  Gaps   0;

Qy   1057 GCTCCGGTGACGCAAGTGCACGATTTTTCGAAACACTCCTGTTTACCGGCCGGCATTGTT 1116
               ||||| ||  || |||| |  ||||:::||     :   :  ::
Db   1042 GCTGCAGTGCGAGGGAGCTTGCGATYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1101
Qy   1117 GCTGGCGTGGGTTTGGGCATTCAGCTTTCTGAAATCTTGCATGTCATGTTGCCTGCCATG 1176
               :: ::  :: :::: ::::::     ::::::::::::::::::
Db   1102 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1161
Qy   1177 GAGTCCGCTGCGCAGCACCTAATTATTCGTCTACATTCGCCCGCATTATCGCTGGTGGCGTC 1236
               ::: ::::::::::::::::::::::::::::::::::::::::::::
Db   1162 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1221
Qy   1237 ACCGCAGCGGCCTTCGCAGTGGGTTGTTACGCGGAGTGTCCTCGGTGATTATTGCGGGG 1296
               ::: :::::::::::::::::::::::::::::::::::::::::::::::
Db   1222 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1281
Qy   1297 CTTACTGCGCTGATGGGTTCTGCGTTTTATTACCTCTTCGTTGTTGTTTATTTAGGCCCCTC 1356
               ::::: :: :  :::: :: ::::::::::::::::::::::::::::::::
Db   1282 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1341
Qy   1357 TCTGCCCGTGCGATTGCTGCAACAGCAGTTGGTTTCACTGGTGGTTTGCTTCGCCCGTCGA 1416
               ::: ::::::::::::::::::::::::::::::::::::::::::::::
Db   1342 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1401
Qy   1417 TTCTTGATTCCACCGTTGATTGTGGCGATTGCCG 1450
               ::::: :::: ::::::::: :: ::: :::||:|
Db   1402 YYYYYYYYYYYYYYYYYYYYYYYYYYYG 1435

RESULT 7
US-08-956-171E-4234/c
;   Sequence 4234, Application US/08956171E
;   Patent No. 6593114
;   GENERAL INFORMATION:
;     APPLICANT: Charles Kunsch
;              Gil H. Choi
;              Patrick S. Dillon
;              Craig A. Rosen
;              Steven C. Barash
;              Michael R. Fannon
;   TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
;   NUMBER OF SEQUENCES: 5256
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: Human Genome Sciences, Inc.
;     STREET: 9410 Key West Avenue
;     CITY: Rockville
;     STATE: Maryland
;     COUNTRY: USA
;     ZIP: 20850
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
;     COMPUTER: HP Vectra 486/33
;     OPERATING SYSTEM: MSDOS version 6.2
;     SOFTWARE: ASCII Text
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/08/956,171E
;     FILING DATE: 20-Oct-1997
;     CLASSIFICATION: <Unknown>
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: 60/009,861
;     FILING DATE: January 5, 1996
;     APPLICATION NUMBER: 08/781,986
;     FILING DATE: January 3, 1997
;   ATTORNEY/AGENT INFORMATION:
;     NAME: Mark J. Hyman
```

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;     REGISTRATION NUMBER: 46,789
;     REFERENCE/DOCKET NUMBER: PB248P1
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: (240) 314-1224
;     TELEFAX: (301) 309-8439
;   INFORMATION FOR SEQ ID NO: 4234:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH: 400 base pairs
;       TYPE: nucleic acid
;       STRANDEDNESS: double
;       TOPOLOGY: linear
;     SEQUENCE DESCRIPTION: SEQ ID NO: 4234:
US-08-956-171E-4234

Query Match        2.4%;  Score 46.6; DB 4;  Length 400;
Best Local Similarity   61.9%;  Pred. No. 0.00022;
Matches  73;  Conservative   0;  Mismatches 45;  Indels   0;  Gaps   0;

Qy     32 ATCCCCCCCTTTGACCTGGTGTTATTGAGCTGGAGAAGAGACTTGAACTCTCAACCTAC 91
              ||| |||  || ||||||   ::: ||||| ||||||||||||||| ||||||||||
Db    298 AGCCCANTCGTTACCCCTCCATAAATGGTGCCGGCGACTTGAACCCCCAACCTAC 239
Qy     92 GCATTACAAGTGCGTTGCGCTGCCAATTGCGCCACTCCAGCACCGCAGATGCTGATGA 149
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    238 TGATTACAAGTGCAGTTGCTTCTACCAATTGAGCTAGGCCGGCTAAGAAATGGTTCAGGA 181

RESULT 8
US-08-781-986A-4234/c
;   Sequence 4234, Application US/08781986A
;   Patent No. 6737248
;   GENERAL INFORMATION:
;     APPLICANT: Charles Kunsch
;   TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
;   NUMBER OF SEQUENCES: 5255
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: Human Genome Sciences, Inc.
;     STREET: 9410 Key West Avenue
;     CITY: Rockville
;     STATE: Maryland
;     COUNTRY: USA
;     ZIP: 20850
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
;     COMPUTER: HP Vectra 486/33
;     OPERATING SYSTEM: MSDOS version 6.2
;     SOFTWARE: ASCII Text
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/08/781,986A
;     FILING DATE:
;     CLASSIFICATION: 435
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:
;     FILING DATE:
;   ATTORNEY/AGENT INFORMATION:
;     NAME: Benson, Bob
;     REGISTRATION NUMBER: 30,446
;     REFERENCE/DOCKET NUMBER: PB248PP
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: (301) 309-8504
;     TELEFAX: (301) 309-8512
;   INFORMATION FOR SEQ ID NO: 4234:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH: 400 base pairs
;       TYPE: nucleic acid
;       STRANDEDNESS: double
;       TOPOLOGY: linear
US-08-781-986A-4234

Query Match        2.4%;  Score 46.6; DB 4;  Length 400;
Best Local Similarity   61.9%;  Pred. No. 0.00022;
Matches  73;  Conservative   0;  Mismatches 45;  Indels   0;  Gaps   0;
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Qy     32 ATCCCCCCCTTTGACCTGGTCTGTTATTGAGCTGGAGAAGAGACTTGAACTCTCAACCTAC 91
          ||| |||| ||  |||         ||||||||||||||||||||||| |||||||||||
Db    298 AGCCCANTCGTTACCCCTCCATAAATGGTGCCGGCCAGAGAGACTTGAACCCCCAACCTAC 239

Qy     92 GCATTACAAGTCGTTGCGCTGCCAATTGCGCCACTCCAGCACCGCAGATGCTGATGA 149
          |||||||| |||||||     |||||| || ||||||||| ||| ||| ||||
Db    238 TGATTACAAGTCAGTTGCTCTACCAATTGAGCTAGGCCGGCTAAGAAATGGTTCAGGA 181


RESULT 9
US-09-198-452A-1

; Sequence 1, Application US/09198452A
; Patent No. 6559294
; GENERAL INFORMATION:
;  APPLICANT: Griffais, R.
;  TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
;  TITLE OF INVENTION:  thereof and uses thereof, in particular for the diagnosis, preve
;  TITLE OF INVENTION:  and treatment of infection
;  FILE REFERENCE: 9710-003-999
;  CURRENT APPLICATION NUMBER: US/09/198,452A
;  CURRENT FILING DATE: 1998-11-24
;  NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 1
;  LENGTH: 1230025
;  TYPE: DNA
;  ORGANISM: Chlamydia pneumoniae
;  FEATURE:
;  NAME/KEY: misc_feature
;  LOCATION: (1)..(15000)
;  OTHER INFORMATION: n=a or c or g or t
;  NAME/KEY: misc_feature
;  LOCATION: (15001)..(30000)
;  OTHER INFORMATION: n=a or c or g or t
;  NAME/KEY: misc_feature
;  LOCATION: (30001)..(45000)
;  OTHER INFORMATION: n=a or c or g or t
;  NAME/KEY: misc_feature
;  LOCATION: (45001)..(60000)
;  OTHER INFORMATION: n=a or c or g or t
;  NAME/KEY: misc_feature
;  LOCATION: (60001)..(75000)
;  OTHER INFORMATION: n=a or c or g or t
;  NAME/KEY: misc_feature
;  LOCATION: (75001)..(90000)
;  OTHER INFORMATION: n=a or c or g or t
;  NAME/KEY: misc_feature
;  LOCATION: (90001)..(105000)
;  OTHER INFORMATION: n=a or c or g or t
;  NAME/KEY: misc_feature
;  LOCATION: (105001)..(120000)
;  OTHER INFORMATION: n=a or c or g or t
;  NAME/KEY: misc_feature
;  LOCATION: (120001)..(135000)
;  OTHER INFORMATION: n=a or c or g or t
;  NAME/KEY: misc_feature
;  LOCATION: (135001)..(150000)
;  OTHER INFORMATION: n=a or c or g or t
;  NAME/KEY: misc_feature
;  LOCATION: (150001)..(165000)
;  OTHER INFORMATION: n=a or c or g or t
;  NAME/KEY: misc_feature
;  LOCATION: (165001)..(180000)
;  OTHER INFORMATION: n=a or c or g or t
;  NAME/KEY: misc_feature
;  LOCATION: (180001)..(195000)
;  OTHER INFORMATION: n=a or c or g or t
;  NAME/KEY: misc_feature
;  LOCATION: (195001)..(210000)
;  OTHER INFORMATION: n=a or c or g or t
;  NAME/KEY: misc_feature
;  LOCATION: (210001)..(225000)
;  OTHER INFORMATION: n=a or c or g or t
;  NAME/KEY: misc_feature
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;  LOCATION: (225001)..(240000)
;  OTHER INFORMATION: n=a or c or g or t
;  NAME/KEY: misc_feature
;  LOCATION: (240001)..(255000)
;  OTHER INFORMATION: n=a or c or g or t
;  NAME/KEY: misc_feature
;  LOCATION: (255001)..(270000)
;  OTHER INFORMATION: n=a or c or g or t
;  NAME/KEY: misc_feature
;  LOCATION: (270001)..(285000)
;  OTHER INFORMATION: n=a or c or g or t
;  NAME/KEY: misc_feature
;  LOCATION: (285001)..(300000)
;  OTHER INFORMATION: n=a or c or g or t
;  NAME/KEY: misc_feature
;  LOCATION: (300001)..(315000)
;  OTHER INFORMATION: n=a or c or g or t
;  NAME/KEY: misc_feature
;  LOCATION: (315001)..(330000)
;  OTHER INFORMATION: n=a or c or g or t
;  NAME/KEY: misc_feature
;  LOCATION: (330001)..(345000)
;  OTHER INFORMATION: n=a or c or g or t
;  NAME/KEY: misc_feature
;  LOCATION: (345001)..(360000)
;  OTHER INFORMATION: n=a or c or g or t
;  NAME/KEY: misc_feature
;  LOCATION: (360001)..(375000)
;  OTHER INFORMATION: n=a or c or g or t
;  NAME/KEY: misc_feature
;  LOCATION: (375001)..(390000)
;  OTHER INFORMATION: n=a or c or g or t
;  NAME/KEY: misc_feature
;  LOCATION: (390001)..(405000)
;  OTHER INFORMATION: n=a or c or g or t
;  NAME/KEY: misc_feature
;  LOCATION: (405001)..(420000)
;  OTHER INFORMATION: n=a or c or g or t
;  NAME/KEY: misc_feature
;  LOCATION: (420001)..(435000)
;  OTHER INFORMATION: n=a or c or g or t
;  NAME/KEY: misc_feature
;  LOCATION: (435001)..(450000)
;  OTHER INFORMATION: n=a or c or g or t
;  NAME/KEY: misc_feature
;  LOCATION: (450001)..(465000)
;  OTHER INFORMATION: n=a or c or g or t
;  NAME/KEY: misc_feature
;  LOCATION: (465001)..(480000)
;  OTHER INFORMATION: n=a or c or g or t
;  NAME/KEY: misc_feature
;  LOCATION: (480001)..(495000)
;  OTHER INFORMATION: n=a or c or g or t
;  NAME/KEY: misc_feature
;  LOCATION: (495001)..(510000)
;  OTHER INFORMATION: n=a or c or g or t
;  NAME/KEY: misc_feature
;  LOCATION: (510001)..(525000)
;  OTHER INFORMATION: n=a or c or g or t
;  NAME/KEY: misc_feature
;  LOCATION: (525001)..(540000)
;  OTHER INFORMATION: n=a or c or g or t
;  NAME/KEY: misc_feature
;  LOCATION: (540001)..(555000)
;  OTHER INFORMATION: n=a or c or g or t
;  NAME/KEY: misc_feature
;  LOCATION: (555001)..(570000)
;  OTHER INFORMATION: n=a or c or g or t
;  NAME/KEY: misc_feature
;  LOCATION: (570001)..(585000)
;  OTHER INFORMATION: n=a or c or g or t
;  NAME/KEY: misc_feature
;  LOCATION: (585001)..(600000)
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; OTHER INFORMATION: n=a or c or g or t
; NAME/KEY: misc_feature
; LOCATION: (600001)..(615000)
; OTHER INFORMATION: n=a or c or g or t
; NAME/KEY: misc_feature
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; OTHER INFORMATION: n=a or c or g or t
; NAME/KEY: misc_feature
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; OTHER INFORMATION: n=a or c or g or t
; NAME/KEY: misc_feature
; LOCATION: (645001)..(660000)
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; NAME/KEY: misc_feature
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; LOCATION: (675001)..(690000)
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; NAME/KEY: misc_feature
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; NAME/KEY: misc_feature
; LOCATION: (720001)..(735000)
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; LOCATION: (750001)..(765000)
; OTHER INFORMATION: n=a or c or g or t
; NAME/KEY: misc_feature
; LOCATION: (765001)..(780000)
; OTHER INFORMATION: n=a or c or g or t
; NAME/KEY: misc_feature
; LOCATION: (780001)..(795000)
; OTHER INFORMATION: n=a or c or g or t
; NAME/KEY: misc_feature
; LOCATION: (795001)..(810000)
; OTHER INFORMATION: n=a or c or g or t
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; LOCATION: (825001)..(840000)
; OTHER INFORMATION: n=a or c or g or t
; NAME/KEY: misc_feature
; LOCATION: (840001)..(855000)
; OTHER INFORMATION: n=a or c or g or t
; NAME/KEY: misc_feature
; LOCATION: (855001)..(870000)
; OTHER INFORMATION: n=a or c or g or t
; NAME/KEY: misc_feature
; LOCATION: (870001)..(885000)
; OTHER INFORMATION: n=a or c or g or t
; NAME/KEY: misc_feature
; LOCATION: (885001)..(900000)
; OTHER INFORMATION: n=a or c or g or t
; NAME/KEY: misc_feature
; LOCATION: (900001)..(915000)
; OTHER INFORMATION: n=a or c or g or t
; NAME/KEY: misc_feature
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Query Match               2.4%;     Score 45.8;  DB 4;  Length 1230025;
Best Local Similarity    76.7%;     Pred. No. 0.046;
Matches  56;  Conservative   0;  Mismatches  17;  Indels    0;  Gaps      0;

Qy      61 GCTGGAGAGAAGAGACTTGAACTCTCAACCTACGCATTACAAGTGCGTTGCGCTGCCAATTG 120
            ||||||||||||||| ||||||||||||||| ||||||||||||||||||||||||||||||
Db  303710 GCTGGAGAAGGAATTGAACCCTCAACCGTTCGATTACAAATCGAATGAATCGAATGCTCTGCCAATTG 303769
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Qy     121 CGCCACTCCAGCA 133
            || ||||||||||
Db  303770 AGCTACTCCAGCA 303782
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RESULT 10
US-08-956-171E-4023
; Sequence 4023, Application US/08956171E
; Patent No. 6593114
; GENERAL INFORMATION:
;   APPLICANT: Charles Kunsch
;   Gil H. Choi
;   Patrick S. Dillon
;   Craig A. Rosen
;   Steven C. Barash
;   Michael R. Fannon
;   TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
;   NUMBER OF SEQUENCES: 5256
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Human Genome Sciences, Inc.
;   STREET: 9410 Key West Avenue
;   CITY: Rockville
;   STATE: Maryland
;   COUNTRY: USA
;   ZIP: 20850
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
;   COMPUTER: HP Vectra 486/33
;   OPERATING SYSTEM: MSDOS version 6.2
;   SOFTWARE: ASCII Text
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/956,171E
;   FILING DATE: 20-Oct-1997
;   CLASSIFICATION: <Unknown>
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: 60/009,861
;   FILING DATE: January 5, 1996
;   APPLICATION NUMBER: 08/781,986
;   FILING DATE: January 3, 1997
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Mark J. Hyman
;   REGISTRATION NUMBER: 46,789
;   REFERENCE/DOCKET NUMBER: PB248P1
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (240) 314-1224
;   TELEFAX: (301) 309-8439
; INFORMATION FOR SEQ ID NO: 4023:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 381 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: double
;   TOPOLOGY: linear
;   SEQUENCE DESCRIPTION: SEQ ID NO: 4023:
US-08-956-171E-4023

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Query Match              2.4%;     Score 45.6;  DB 4;  Length 381;
Best Local Similarity   73.1%;     Pred. No. 0.00043;
Matches  57;  Conservative   0;  Mismatches  21;  Indels    0;  Gaps      0;

Qy      56 ATTGAGCTGGAGAAGAGACTTGAACTCTCAACCTACGCATTACAAGTGCGTTGCGCTGCC 115
            ||||||||||||||||| |||||||| ||||||||||||||||||||||||||||||||||
Db      87 ATGGNGCNGGCCAGAGACTTGAACCCCCAACCTACTACTGATTACAAGTCAGTTGCTCTACC 146

Qy     116 AATTGCGCCACTCCAGCA 133
            ||||||||||||||||||
Db     147 AATTGAGCTAGGCCGGCA 164
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RESULT 11
US-08-781-986A-4023
; Sequence 4023, Application US/08781986A
; Patent No. 6737248

GENERAL INFORMATION:
APPLICANT: Charles Kunsch
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5255
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/781,986A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Benson, Bob
REGISTRATION NUMBER: 30,446
REFERENCE/DOCKET NUMBER: PB248PP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 4023:
SEQUENCE CHARACTERISTICS:
LENGTH: 381 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
US-08-781-986A-4023

Query Match   2.4%;   Score 45.6; DB 4; Length 381;
Best Local Similarity 73.1%; Pred. No. 0.00043;
Matches 57; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

Qy   56 ATTGAGCTGGAGAAGAGACTTGAACTCTCAACCTACCGCATTACAAGTGCGTTGCGCTGCC 115
        ||| || ||||||||||||||||||||| ||||||||| |||||||||| ||||| ||
Db   87 ATGGNGCNGGCCAGAGAGACTTGAACCCCCCAACCTACTGATTACAAGTCAGTTGCTCTACC 146

Qy 116 AATTGCGCCACTCCAGCA 133
        ||||| || ||| ||
Db 147 AATTGAGCTAGGCCGGCA 164

RESULT 12
US-08-956-171E-4566
; Sequence 4566, Application US/08956171E
; Patent No. 6593114
; GENERAL INFORMATION:
APPLICANT: Charles Kunsch
          Gil H. Choi
          Patrick S. Dillon
          Craig A. Rosen
          Steven C. Barash
          Michael R. Fannon
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5256
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/956,171E
FILING DATE: 20-Oct-1997
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/009,861
FILING DATE: January 5, 1996
APPLICATION NUMBER: 08/781,986
FILING DATE: January 3, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Mark J. Hyman
REGISTRATION NUMBER: 46,789
REFERENCE/DOCKET NUMBER: PB248P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (240) 314-1224
TELEFAX: (301) 309-8439
INFORMATION FOR SEQ ID NO: 4566:
SEQUENCE CHARACTERISTICS:
LENGTH: 237 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 4566:
US-08-956-171E-4566

Query Match   2.3%;   Score 44.4; DB 4; Length 237;
Best Local Similarity 73.1%; Pred. No. 0.00078;
Matches 57; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

Qy   56 ATTGAGCTGGAGAAGAGACTTGAACTCTCAACCTACCGCATTACAAGTGCGTTGCGCTGCC 115
        ||| || ||||||||||||||||||||| ||||||||| |||||||||| ||||| ||
Db   25 ATGGTGCGCCAGAGAGACTTGAACCCCAACCCAACCTACTGATTACAAGTCAGTTGCTCTACC 84

Qy 116 AATTGCGCCACTCCAGCA 133
        ||||| || ||| ||
Db   85 AATTGAGCTAGGCCGGCA 102

RESULT 13
US-08-781-986A-4566
; Sequence 4566, Application US/08781986A
; Patent No. 6737248
; GENERAL INFORMATION:
APPLICANT: Charles Kunsch
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5255
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/781,986A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Benson, Bob
REGISTRATION NUMBER: 30,446
REFERENCE/DOCKET NUMBER: PB248PP
TELECOMMUNICATION INFORMATION:

```
;   TELEPHONE: (301) 309-8504
;   TELEFAX:   (301) 309-8512
; INFORMATION FOR SEQ ID NO: 4566:
;  SEQUENCE CHARACTERISTICS:
;   LENGTH: 237 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: double
;   TOPOLOGY: linear
US-08-781-986A-4566

Query Match          2.3%;   Score 44.4;  DB 4;   Length 237;
Best Local Similarity  73.1%;  Pred. No. 0.00078;
Matches   57;  Conservative   0;  Mismatches  21;  Indels   0;  Gaps   0;

Qy      56 ATTGAGCTGGAGAAGAGACTTGAACTCTCAACCTACGCATTACAAGTGCGTTGCGCTGCC 115
           |||||||||||||||||| |||||||||| |||||||| |||||||| ||||||| |||
Db      25 ATGGTGCGCCGCCAGAGGACTTGAACCCCCAACCTACTGATTACAAGTCAGTTGCTCTACC 84

Qy     116 AATTGCGCCACTCCAGCA 133
           |||| |||| ||
Db      85 AATTGAGCTAGGCCGGCA 102


RESULT 14
US-08-956-171E-4543
; Sequence 4543, Application US/08956171E
; Patent No. 6593114
; GENERAL INFORMATION:
;  APPLICANT: Charles Kunsch
;             Gil H. Choi
;             Patrick S. Dillon
;             Craig A. Rosen
;             Steven C. Barash
;             Michael R. Fannon
;  TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
;  NUMBER OF SEQUENCES: 5256
;  CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Human Genome Sciences, Inc.
;   STREET: 9410 Key West Avenue
;   CITY: Rockville
;   STATE: Maryland
;   COUNTRY: USA
;   ZIP: 20850
;  COMPUTER READABLE FORM:
;   MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
;   COMPUTER: HP Vectra 486/33
;   OPERATING SYSTEM: MSDOS version 6.2
;   SOFTWARE: ASCII Text
;  CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/956,171E
;   FILING DATE: 20-Oct-1997
;   CLASSIFICATION: <Unknown>
;  PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: 60/009,861
;   FILING DATE: January 5, 1996
;   APPLICATION NUMBER: 08/781,986
;   FILING DATE: January 3, 1997
;  ATTORNEY/AGENT INFORMATION:
;   NAME: Mark J. Hyman
;   REGISTRATION NUMBER: 46,789
;   REFERENCE/DOCKET NUMBER: PB248P1
;   TELECOMMUNICATION INFORMATION:
;    TELEPHONE: (240) 314-1224
;    TELEFAX:   (301) 309-8439
; INFORMATION FOR SEQ ID NO: 4543:
;  SEQUENCE CHARACTERISTICS:
;   LENGTH: 239 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: double
;   TOPOLOGY: linear
;  SEQUENCE DESCRIPTION: SEQ ID NO: 4543:
US-08-956-171E-4543


Query Match          2.3%;   Score 44.4;  DB 4;   Length 239;
Best Local Similarity  73.1%;  Pred. No. 0.00079;
Matches   57;  Conservative   0;  Mismatches  21;  Indels   0;  Gaps   0;

Qy      56 ATTGAGCTGGAGAAGAGACTTGAACTCTCAACCTACGCATTACAAGTGCGTTGCGCTGCC 115
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RESULT 15
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; Sequence 4544, Application US/08956171E
; Patent No. 6593114
; GENERAL INFORMATION:
;  APPLICANT: Charles Kunsch
;             Gil H. Choi
;             Patrick S. Dillon
;             Craig A. Rosen
;             Steven C. Barash
;             Michael R. Fannon
;  TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
;  NUMBER OF SEQUENCES: 5256
;  CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Human Genome Sciences, Inc.
;   STREET: 9410 Key West Avenue
;   CITY: Rockville
;   STATE: Maryland
;   COUNTRY: USA
;   ZIP: 20850
;  COMPUTER READABLE FORM:
;   MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
;   COMPUTER: HP Vectra 486/33
;   OPERATING SYSTEM: MSDOS version 6.2
;   SOFTWARE: ASCII Text
;  CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/956,171E
;   FILING DATE: 20-Oct-1997
;   CLASSIFICATION: <Unknown>
;  PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: 60/009,861
;   FILING DATE: January 5, 1996
;   APPLICATION NUMBER: 08/781,986
;   FILING DATE: January 3, 1997
;  ATTORNEY/AGENT INFORMATION:
;   NAME: Mark J. Hyman
;   REGISTRATION NUMBER: 46,789
;   REFERENCE/DOCKET NUMBER: PB248P1
;   TELECOMMUNICATION INFORMATION:
;    TELEPHONE: (240) 314-1224
;    TELEFAX:   (301) 309-8439
; INFORMATION FOR SEQ ID NO: 4544:
;  SEQUENCE CHARACTERISTICS:
;   LENGTH: 239 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: double
;   TOPOLOGY: linear
;  SEQUENCE DESCRIPTION: SEQ ID NO: 4544:
US-08-956-171E-4544


Query Match          2.3%;   Score 44.4;  DB 4;   Length 239;
Best Local Similarity  73.1%;  Pred. No. 0.00079;
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us-09-963-521-3.rni

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Job time : 176.998 secs

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                    GenCore version 5.1.6

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OM nucleic - nucleic search, using sw model

Run on:      January 14, 2005, 09:56:14  ; Search time 969.85 Seconds
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                 Gapop 10.0 , Gapext 1.0

Searched:        4300275 seqs, 2872944193 residues

Total number of hits satisfying chosen parameters:      8600550

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	1909	100.0	1909	9	US-09-963-521-3	Sequence 3, Appli
3	1909	100.0	1909	9	US-09-834-721-3	Sequence 3, Appli
4	1909	100.0	1909	10	US-09-783-388-3	Sequence 3, Appli
5	1909	100.0	1909	9	US-09-951-535-3	Sequence 11, Appli
6	1909	100.0	1909	17	US-10-224-574-11	Sequence 1, Appli
7	1865.4	97.7	3309400	9	US-09-738-626-1	Sequence 1, Appli
8	1836.6	96.2	2817	9	US-09-951-536-1	Sequence 1, Appli
9	1836.6	96.2	2817	9	US-09-963-521-1	Sequence 1, Appli
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ALIGNMENTS

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RESULT 1
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; Sequence 3, Application US/09951536
; Patent No. US2002010737BA1
; GENERAL INFORMATION:
;  APPLICANT: ZIEGLER, PETRA
;  APPLICANT: EGGELING, LOTHAR
;  APPLICANT: SAHM, HERMANN
;  APPLICANT: THIERBACH, GEORG
;  TITLE OF INVENTION: NEW NUCLEOTIDE SEQUENCES CODING FOR THE THRE GENE AND
;  TITLE OF INVENTION: PROCESS FOR THE ENZYMATIC PRODUCTION OF L-THREONINE
;  TITLE OF INVENTION: USING CORYNEFORM BACTERIA
; FILE REFERENCE: 21123/282414/MAS
; CURRENT APPLICATION NUMBER: US/09/951,536
; CURRENT FILING DATE: 2001-09-14
; PRIOR APPLICATION NUMBER: 09/431,099
; PRIOR FILING DATE: 1999-11-01
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
;  LENGTH: 1909
;  TYPE: DNA
;  ORGANISM: Corynebacterium glutamicum
;  FEATURE:
;  NAME/KEY: CDS
;  LOCATION: (280)..(1746)
;  OTHER INFORMATION: thrB-Gen
US-09-951-536-3

Query Match             100.0%;  Score 1909;  DB 9;  Length 1909;
Best Local Similarity   100.0%;  Pred. No. 0;
Matches 1909;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

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; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 1909
; TYPE: DNA
; ORGANISM: Corynebacterium glutanicum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (280)..(1746)
; OTHER INFORMATION: thrB-Gen
US-09-963-521-3

Query Match      100.0%;   Score 1909;   DB 9;   Length 1909;
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Db  901 GGTGGTTTTATTGCCACGCGTCCGTGCCTGCATCGATTGCTTATTCTTTGGCGTGCAATTTGGT  960

Qy  961 CTTGAGATCAAACCGAGCCAGATCATCGCATCTGGAATTGTGTGCGTGTCGTGTGGCAGGTTTG  1020
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Db  961 CTTGAGATCAAACCGAGCCAGATCATCGCATCTGGAATTGTGTGCGTGTCGTGTGGCAGGTTTG  1020

Qy 1021 ACACTCGTCGAATCTCTGCGAGGACGGCATCACGGCGCTCCGGTGACAGCAGTGCACGA  1080
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Db 1021 ACACTCGTCGAATCTCTGCGAGGACGGCATCACGGCGCTCCGGTGACAGCAGTGCACGA  1080

Qy 1081 TTTTTCGAAACACTCCTGTTTACCGGCGGCATTGTTGCTGGCGTGGGTTGGGCATTCAG  1140
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Db 1081 TTTTTCGAAACACTCCTGTTTACCGGCGGCATTGTTGCTGGCGTGGGTTGGGCATTCAG  1140

Qy 1141 CTTTCTGAAATCTTGCATGTCATGTGCCTGCCATGGAGTCCGCTGCAGCACCTAATTAT  1200
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Db 1141 CTTTCTGAAATCTTGCATGTCATGTGCCTGCCATGGAGTCCGCTGCAGCACCTAATTAT  1200

Qy 1201 TCGTCTACATTCGCCCGCATTATCGCTGGTGGCGTCACCGCAGCCGGCCCTTCGCAGTGGGT  1260
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Db 1201 TCGTCTACATTCGCCCGCATTATCGCTGGTGGCGTCACCGCAGCCGGCCCTTCGCAGTGGGT  1260

Qy 1261 TGTTACGCGGAGTGGTCCTCGGTGATTATTGCGGGGCTTACTGCGCGTGATGGGTTCTGCG  1320
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Db 1261 TGTTACGCGGAGTGGTCCTCGGTGATTATTGCGGGGCTTACTGCGCGTGATGGGTTCTGCG  1320

Qy 1321 TTTTATTACCTCTTCGTTGTGTTATTTAGGCCCCGTCTCTCGCCGTCCGCGGATTGCTGCAACA  1380
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Db 1321 TTTTATTACCTCTTCGTTGTGTTATTTAGGCCCCGTCTCTCGCCGTCCGCGGATTGCTGCAACA  1380

Qy 1381 GCAGTTGGTTTCACTGGTGGTTGCCGTGTGATTCCTGATTCCTGTTGATTGTG  1440
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1381 GCAGTTGGTTTCACTGGTGGTTGCCGTGTGATTCCTGATTCCTGTTGATTGTG  1440

Qy 1441 GCGATTGCCGGCGCATCACACCAATGCTTCCAGGTCTGCAATTTACCGCGGAATGTACGCC  1500
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Db 1441 GCGATTGCCGGCGCATCACACCAATGCTTCCAGGTCTGCAATTTACCGCGGAATGTACGCC  1500

Qy 1501 ACCCTGAATGATCAAACACTCATGGGTTCACCAACATTGCGGTTGCTTTAGCCACTGCT  1560
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1501 ACCCTGAATGATCAAACACTCATGGGTTCACCAACATTGCGGTTGCTTTAGCCACTGCT  1560

Qy 1561 TCATCACTTGCCGCTGCCGGTGGTTTGGGTGAGTTGGGGTGAGTTGCCCGAGGCTACGTCGTCCA  1620
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Db 1561 TCATCACTTGCCGCTGCCGGTGGTTTGGGTGAGTTGGGGTGAGTTGCCCGAGGCTACGTCGTCCA  1620

Qy 1621 CCACGCTTCAACCCATACCGTGCATTTACCGCTTCAACCGCAATGAGTTCTCCTTCCAGGAGGAA  1680
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Db 1621 CCACGCTTCAACCCATACCGTGCATTTACCGCTTCAACCGCAATGAGTTCTCCTTCCAGGAGGAA  1680

Qy 1681 GCTGAGCAGAATCAGCGCGCCGCCGCAGAGAAAACGTCCAAAGACTAATCAGAGATTCGGTAAT  1740
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Db 1681 GCTGAGCAGAATCAGCGCGCCGCCGCAGAGAAAACGTCCAAAGACTAATCAGAGATTCGGTAAT  1740

Qy 1741 AAAAGGTAAAAATCAACCTGCTTAGGCGTCTTTCGCTTAAATAGCGTAGAATATCGGGTC  1800
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Db 1741 AAAAGGTAAAAATCAACCTGCTTAGGCGTCTTTCGCTTAAATAGCGTAGAATATCGGGTC  1800

Qy 1801 GATCGCTTTTAAACACTCAGGAGGATCCTTGCCGCGGCCAAAATCACCGGACACTCGTCCCAC  1860
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1801 GATCGCTTTTAAACACTCAGGAGGATCCTTGCCGCGGCCAAAATCACCGGACACTCGTCCCAC  1860

Qy 1861 CCCAGAATCCCTTCACGCTTGTTGAAGAGGAAACCGCAGCCGGGGTACCG  1909
Db 1861 CCCAGAATCCCTTCACGCTTGTTGAAGAGGAAACCGCAGCCGGGGTACCG  1909
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RESULT 3
US-09-834-721-3
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; Sequence 3, Application US/09834721
; Patent No. US20020155551A1
; GENERAL INFORMATION:
;   APPLICANT: RIEPING, MECHTHILD
;   TITLE OF INVENTION: PROCESS FOR THE FERMENTATIVE PREPARATION OF L-THREONINE
;   FILE REFERENCE: 21123/280169/MAS
;   CURRENT APPLICATION NUMBER: US/09/834,721
;   CURRENT FILING DATE: 2001-04-16
;   PRIOR APPLICATION NUMBER: DE 100 26 494.8
;   PRIOR FILING DATE: 2000-05-27
;   PRIOR APPLICATION NUMBER: DE 101 02 823.7
;   PRIOR FILING DATE: 2001-01-23
;   NUMBER OF SEQ ID NOS: 12
;   SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
;   LENGTH: 1909
;   TYPE: DNA
;   ORGANISM: Corynebacterium glutamicum
;   FEATURE:
;   OTHER INFORMATION: ATCC13032
;   NAME/KEY: CDS
;   LOCATION: (280)..(1746)
;   OTHER INFORMATION: thrE gene
US-09-834-721-3

Query Match          100.0%;   Score 1909;  DB 9;   Length 1909;
Best Local Similarity 100.0%;  Pred. No. 0;
Matches 1909;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;
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Qy         1 AGCTTGCATGCTGCGACTCTAGAGGATCCCCCCCCTTTGACCTGGTGTTATTGA    60
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Db         1 AGCTTGCATGCTGCGACTCTAGAGGATCCCCCCCCTTTGACCTGGTGTTATTGA    60

Qy        61 GCTGGAGAAGAGACTTGAACTCTCAACTACGTGCGTTGCGCCAATTG   120
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Db        61 GCTGGAGAAGAGACTTGAACTCTCAACTACGTGCGTTGCGCCAATTG   120

Qy       121 CGCCACTCCAGCACCCAGAGTGCTGATGATCAACAACTACGAATACGTATCTTAGCGTAT   180
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Db       121 CGCCACTCCAGCACCCAGAGTGCTGATGATCAACAACTACGAATACGTATCTTAGCGTAT   180

Qy       181 GTGTACATCACAATGGAATTCGGGGCTAGAGTATCTGGTGAACCGTTGCATAAACGACCTG   240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       181 GTGTACATCACAATGGAATTCGGGGCTAGAGTATCTGGTGAACCGTTGCATAAACGACCTG   240

Qy       241 TGATTGGACTCTTTTCCTTGCAAAATGTTTTCCAGCGGATGTTGAGTTTTGCGACCCTT   300
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Db       241 TGATTGGACTCTTTTCCTTGCAAAATGTTTTCCAGCGGATGTTGAGTTTTGCGACCCTT   300

Qy       301 CGTGGCCGCATTCAACAGTTGACGCTGCAAAAGCCGCACCTCCGCGCCACTCCGCCACTAGCC   360
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Db       301 CGTGGCCGCATTCAACAGTTGACGCTGCAAAAGCCGCACCTCCGCGCCACTCCGCCACTAGCC   360

Qy       361 CCGATTGATCTCACTACTGACCATAGTCAAGTGGCCGGTGTGATGAATTGGCTGCGAGAATT   420
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Db       361 CCGATTGATCTCACTACTGACCATAGTCAAGTGGCCGGTGTGATGAATTGGCTGCGAGAATT   420

Qy       421 GGGGATATTTGCTTCTTCAGTACGTCAAATAGTGACACCAAGTACAAGTTCGAGCA   480
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Db       421 GGGGATATTTGCTTCTTCAGTACGTCAAATAGTGACACCAAGTACAAGTTCGAGCA   480

Qy       481 GTGACCTCTGCCGTACGGTTTGTACTACACGCACGTGAATACGTTGAATACGATCACC   540
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Db       481 GTGACCTCTGCCGTACGGTTTGTACTACACGCACGTGAATACGTTGAATACGATCACC   540

Qy       541 ATCTTCACCAACATCGGTGTGTGGAGAGAAGAGATGCCGGTCAACGTGTTTCATGTTGTAGGC   600
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Db       541 ATCTTCACCAACATCGGTGTGTGGAGAGAAGAGATGCCGGTCAACGTGTTTCATGTTGTAGGC   600

Qy       601 AAGTTGGACACCAACTTCTCCAAACTGTCTGAGGTTGACCGTTTGATCCGTTCCATTCAG   660
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Db       601 AAGTTGGACACCAACTTCTCCAAACTGTCTGAGGTTGACCGTTTGATCCGTTCCATTCAG   660
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Qy       661 GCTGGTGCGACCCGCCTGAGGTTGCCGAGAAATCCTGGACGAGTTGGAGCAATCCCT   720
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Db       661 GCTGGTGCGACCCGCCTGAGGTTGCCGAGAAATCCTGGACGAGTTGGAGCAATCCCT   720

Qy       721 GCGTCTTATGGTTTCCCGTGTGCGTTGCGGCTGGGCAATGATGGGTGGTGCTGTTGCT   780
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Db       721 GCGTCTTATGGTTTCCCGTGTGCGTTGCGGCTGGGCAATGATGGGTGGTGCTGTTGCT   780

Qy       781 GTGCTGTGGTGGTGTGGATGGCAGGTTCCCTAATGTCTTTATTACCGCCGTTCACGATC   840
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Db       781 GTGCTGTGGTGGTGTGGATGGCAGGTTCCCTAATGTCTTTATTACCGCCGTTCACGATC   840

Qy       841 ATTGCCACGACGTCATTTTGGAAAGAAGGGTTTGCCTACTTTCTTCCAAAATGTTGTT   900
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Db       841 ATTGCCACGACGTCATTTTGGAAAGAAGGGTTTGCCTACTTTCTTCCAAAATGTTGTT   900

Qy       901 GGTGGTTTATTGCCACGCTGCCTGCTGATTGCTATTCTTTGGCGTTGCAATTTGGT   960
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Db       901 GGTGGTTTATTGCCACGCTGCCTGCTGATTGCTATTCTTTGGCGTTGCAATTTGGT   960

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Db      1021 ACACTCGTGCAATCTCTGCAGGACGGCATCACGGGCGCGTCCGGTGACAGCAAGTGCACGA   1080

Qy      1081 TTTTTCGAAAACACTCCTGTTTACCGGCGGCATTGTTGCTGGCGTGGCGTGGTTTGGGCATTCAG   1140
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Db      1081 TTTTTCGAAAACACTCCTGTTTACCGGCGGCATTGTTGCTGGCGTGGCGTGGTTTGGGCATTCAG   1140

Qy      1141 CTTTCTGAAATCTTGACATGTCATGTTGCCTGCGAGTGCTCGCTGCGAGCACCTAATTAT   1200
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Db      1141 CTTTCTGAAATCTTGACATGTCATGTTGCCTGCGAGTGCTCGCTGCGAGCACCTAATTAT   1200

Qy      1201 TCGTCTACATTGCCCCGCCATTATCGCTGGTGGTGCGATTATCGCACCGCGGCCTTCGCAGTGGGT   1260
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Qy      1261 TGTTACGGCGGAGTGGTCCTCGGTGATTATTGGGGGCTTACTGCGCTTGATGGGTTCTGCG   1320
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Db      1261 TGTTACGGCGGAGTGGTCCTCGGTGATTATTGGGGGCTTACTGCGCTTGATGGGTTCTGCG   1320

Qy      1321 TTTTATTACCTCCTTCGTTGTGTTATTTAGGCCCCGTCTCTCGCGCTGGATTGCTGCAACA   1380
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Db      1321 TTTTATTACCTCCTTCGTTGTGTTATTTAGGCCCCGTCTCTCGCGCTGGATTGCTGCAACA   1380

Qy      1381 GCAGTTGGTTCACTGGTGGTTTGCTTGCCCGTGCGCCACTCCCGCCGCCACTAGCC   1440
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1381 GCAGTTGGTTCACTGGTGGTTTGCTTGCCCGTGCGCCACTCCCGCCGCCACTAGCC   1440

Qy      1441 GGGATTGCCGGCATCACACCAATGCTCTAGCAATGCTCTAGCAATTTACCGCGGAATGTACGCC   1500
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Db      1441 GGGATTGCCGGCATCACACCAATGCTCTAGCAATGCTCTAGCAATTTACCGCGGAATGTACGCC   1500

Qy      1501 ACCCTGAATGATCAAACACTCATGGGTTCACCAAGTTGCGGTTGCTTTAGCCACTGCTCTT   1560
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Db      1501 ACCCTGAATGATCAAACACTCATGGGTTCACCAAGTTGCGGTTGCTTTAGCCACTGCTCTT   1560

Qy      1561 TCATCACTTGCCGCTGGCGTGGTTTTGGGTGAGTGATTGCCCAGCTACGTCGTCCA   1620
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Db      1561 TCATCACTTGCCGCTGGCGTGGTTTTGGGTGAGTGATTGCCCAGCTACGTCGTCCA   1620

Qy      1621 CCACGCTTCAACCCATACGGTCATTACCACGGCGAATGAGTTGAGTTCTCCTTCCAGGAGGAA   1680
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Qy      1681 GCTGAGCAGAATCAGCCGCGCGGCAGAGAAAACGTCAAAGACTAATCAGAGATTCGGTAAT   1740
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Db      1681 GCTGAGCAGAATCAGCCGCGCGGCAGAGAAAACGTCAAAGACTAATCAGAGATTCGGTAAT   1740

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Db  1741 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy  1801 GATGCGTTTAAACACTCAGGAGGATCCTTGCCGGCGGCCAAAATCACGGACACTCGTCCCAC 1860
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Db  1801 GATGCGTTTAAACACTCAGGAGGATCCTTGCCGGCGGCCAAAATCACGGACACTCGTCCCAC 1860

Qy  1861 CCCAGAATCCCTTCACGGCTGTTGAAGAGGAAACCGCAGCCGGGGTACCG 1909
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Db  1861 CCCAGAATCCCTTCACGGCTGTTGAAGAGGAAACCGCAGCCGGGGTACCG 1909

RESULT 4
US-09-783-388-3
; Sequence 3, Application US/09783388
; Patent No. US20020016873A1
; GENERAL INFORMATION:
;  APPLICANT: Ziegler, Petra
;  APPLICANT:  Eggeling, Lothar
;  APPLICANT:  Sahm, Hermann
;  APPLICANT:  Thierbach, Georg
;  TITLE OF INVENTION: NEW NUCLEOTIDE SEQUENCES CODING FOR THE THRE GENE AND
;  TITLE OF INVENTION:  PROCESS FOR
;  TITLE OF INVENTION:  ENZYMATIC PRODUCTION OF L-THREONINE USING CORYNEFORM BACTERIA
;  FILE REFERENCE: 21123/277066
;  CURRENT APPLICATION NUMBER: US/09/783,388
;  CURRENT FILING DATE:  2001-02-15
;  NUMBER OF SEQ ID NOS: 8
;  SOFTWARE: Patentin version 3.0
; SEQ ID NO 3
;  LENGTH: 1909
;  TYPE: DNA
;  ORGANISM: Corynebacterium glutamicum ATCC13032
;  FEATURE:
;  NAME/KEY: CDS
;  LOCATION: (280)..(1746)
US-09-783-388-3

Query Match     100.0%;  Score 1909;  DB 9;  Length 1909;
Best Local Similarity  100.0%;  Pred. No. 0;
Matches 1909;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;
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Qy    1 AGCTTGCATGCCATGCCGACTCGAGTCGACTCTAGAGGATCCCCCCCCTTGACCTGGTGTTATTGA 60
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Db    1 AGCTTGCATGCCATGCCGACTCGAGTCGACTCTAGAGGATCCCCCCCCTTGACCTGGTGTTATTGA 60

Qy   61 GCTGGAGAAGAGACTTGAACTCTCAACCTACGCATTACAAGTGCGTTGCGCTGCCAATTG 120
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Qy  121 CGCCACTCCAGCACCGCAGATGCTGATGATCAACAACTACGAATACGTATCTTAGCGTAT 180
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Qy  181 GTGTACATCACAATGGAATTCGGGGCTAGAGTATCTGTGACCGTGCATAAACGACCTG 240
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Qy  241 TGATTGGACTCTTTTCCTTGCAAAATGTTTTCCAGCGGATGTTGAGTTTTGCGACCCTT 300
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Qy  301 CGTGGGCCGCATTCAACAGTTGACGCTGCAAAAGCCCGGTCAAGTGGCCGCCATCGCCACTAGCC 360
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  301 CGTGGGCCGCATTCAACAGTTGACGCTGCAAAAGCCCGGTCAAGTGGCCGCCATCGCCACTAGCC 360

Qy  361 CCGATTGATCTCACTGACCATAGTCAAGTCAAGTGCAAATAGTGACACCAAGGTACAAGTTCGAGCA 420
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Db  361 CCGATTGATCTCACTGACCATAGTCAAGTCAAGTGCAAATAGTGACACCAAGGTACAAGTTCGAGCA 420

Qy  421 GGCGATATTTTGCTTTCTTTGCTTTCTTCTTCAGTGACGTACGTCAAATAGTGCACCAAGGTACAAGTTCGAGCA 480
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Db  421 GGCGATATTTTGCTTTCTTTGCTTTCTTCTTCAGTGACGTACGTCAAATAGTGCACCAAGGTACAAGTTCGAGCA 480
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Qy  481 GTGACCTCTGCGTACGGTTGTACTACACGCACGTGGATATCACGTTGAATACGATCACC 540
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Db  481 GTGACCTCTGCGTACGGTTGTACTACACGCACGTGGATATCACGTTGAATACGATCACC 540

Qy  541 ATCTTCACCAACATCGGTGGTGGAGGAGGAGGAAGATGCCGGTCAACGTGTTCATGTGTTGTAGGC 600
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Db  541 ATCTTCACCAACATCGGTGGTGGAGGAGGAGGAAGATGCCGGTCAACGTGTTCATGTGTTGTAGGC 600

Qy  601 AAGTTGGACACCAACTTCTCCAAACTGTCTGAGGTTGACCGTTGATCCGTTCATTCAG 660
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Db  601 AAGTTGGACACCAACTTCTCCAAACTGTCTGAGGTTGACCGTTGATCCGTTCATTCAG 660

Qy  661 GCTGGTGCGACCCCGCCTGAGGTTGCCGAGAAAATCCTGGACGAGTTGGAGCAATCCCT 720
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Db  661 GCTGGTGCGACCCCGCCTGAGGTTGCCGAGAAAATCCTGGACGAGTTGGAGCAATCCCT 720

Qy  721 GCGGCTTATGGTTCCCTGCTGGCTGGGCAATGATGGGTGCGTGTGTGCT 780
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Db  721 GCGGCTTATGGTTCCCTGCTGGCTGGGCAATGATGGGTGCGTGTGTGCT 780

Qy  781 GTGCTGTGGGTGGTGGTGGTGGAGGTGGCAGGTTCCCTAATTGCTTTTATTACCGGTTCACGATC 840
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Db  781 GTGCTGTGGGTGGTGGTGGTGGAGGTGGCAGGTTCCCTAATTGCTTTTATTACCGGTTCACGATC 840

Qy  841 ATTGCCACGACGTCATTTTTGGGAAAGAAGAGGGTTTGCCTACTTTCTTCCAAAATGTTGTT 900
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Db  841 ATTGCCACGACGTCATTTTTGGGAAAGAAGAGGGTTTGCCTACTTTCTTCCAAAATGTTGTT 900

Qy  901 GGTGGTTTTATTGCCACGGTGCCTGCATCGATTGCTGATTGCTTATTCTTTGGCGTTGCAATTGGT 960
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Db  901 GGTGGTTTTATTGCCACGGTGCCTGCATCGATTGCTGATTGCTTATTCTTTGGCGTTGCAATTGGT 960

Qy  961 CTTGAGATCAAACCAGGCCAGATCATCGAGAATTGTGTGTCTGTGGCAGTTTG 1020
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Db  961 CTTGAGATCAAACCAGGCCAGATCATCGAGAATTGTGTGTCTGTGGCAGTTTG 1020

Qy 1021 ACACTCGTGCAATCTCTGCAGGACGGCATCACGGCGCTCCGGTGACAGCAAGTGCACGA 1080
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Db 1021 ACACTCGTGCAATCTCTGCAGGACGGCATCACGGCGCTCCGGTGACAGCAAGTGCACGA 1080

Qy 1081 TTTTTCGAAACACTCCCTGTTACCGGCCATTGTGCTGGCCATTGTTGGGCATTCAG 1140
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Db 1081 TTTTTCGAAACACTCCCTGTTACCGGCCATTGTGCTGGCCATTGTTGGGCATTCAG 1140

Qy 1141 CTTTCTGAAATCTTGCATGTCATGTGCCTGCAGGAGTCCGCTGCAGCACCTAATTAT 1200
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Db 1141 CTTTCTGAAATCTTGCATGTCATGTGCCTGCAGGAGTCCGCTGCAGCACCTAATTAT 1200

Qy 1201 TCGTCTACATTCGCCCGCATTATCGCTGGTGGCGTCACCGCAGCCGCCTTCGCAGTGGGT 1260
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Db 1201 TCGTCTACATTCGCCCGCATTATCGCTGGTGGCGTCACCGCAGCCGCCTTCGCAGTGGGT 1260

Qy 1261 TGTTACGGCGAGTGGTCCTCGGGTGATTATTGCGGGGCTTACTGCGCTGCCGCGTCTCGCG 1320
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1261 TGTTACGGCGAGTGGTCCTCGGGTGATTATTGCGGGGCTTACTGCGCTGCCGCGTCTCGCG 1320

Qy 1321 TTTTATTACCTCTTCGTTGTTATTTATTGGAGCCCCGTCTCCTGCGCGCTGGATTGCTGCAACA 1380
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1321 TTTTATTACCTCTTCGTTGTTATTTATTGGAGCCCCGTCTCCTGCGCGCTGGATTGCTGCAACA 1380

Qy 1381 GCAGTTGGTTTCACTGGGTGGTTTGCTTGCCCGTCGATTCTGATTCCACCGTTGATTGTG 1440
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1381 GCAGTTGGTTTCACTGGGTGGTTTGCTTGCCCGTCGATTCTGATTCCACCGTTGATTGTG 1440

Qy 1441 GCGATTGCCGGCATCACACCAATGCTTCCCGGTCAGGTTCAGCAATTTACCGCGGAATGTACGCC 1500
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1441 GCGATTGCCGGCATCACACCAATGCTTCCCGGTCAGGTTCAGCAATTTACCGCGGAATGTACGCC 1500

Qy 1501 ACCCTGAATGATCAAACACTCATGGGTTTCACCAACATTGCGGTTGCTTTAGCCACTGCT 1560
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1501 ACCCTGAATGATCAAACACTCATGGGTTTCACCAACATTGCGGTTGCTTTAGCCACTGCT 1560
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Qy   1561 TCATCACTTGCCGCGCTGGCTGGTTGGGTGAGTGGATGCCGCGAGGCTACGTCGTCCA 1620
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1561 TCATCACTTGCCGCGCTGGCTGGTTGGGTGAGTGGATGCCGCGAGGCTACGTCGTCCA 1620

Qy   1621 CCACGCTTCAACCACCATACCGTCGCATTGCATTTACCAAGGCGAATGAGTTCCTTCCAGGAGGAA 1680
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1621 CCACGCTTCAACCACCCATACCGTCGCATTGCATTTACCAAGGCGAATGAGTTCCTTCCAGGAGGAA 1680

Qy   1681 GCTGAGCAGAATCAGCGGCCGGCGAGAAAAGTCCAAAGACTAATCAGAGATTCGGTAAT 1740
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1681 GCTGAGCAGAATCAGCGGCCGGCGAGAAAAGTCCAAAGACTAATCAGAGATTCGGTAAT 1740

Qy   1741 AAAAGGTAAAAATCAACCTGCTTAGGCGTCTTTCGCTTAAATAGGCGTAGATATCGGGTC 1800
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1741 AAAAGGTAAAAATCAACCTGCTTAGGCGTCTTTCGCTTAAATAGGCGTAGATATCGGGTC 1800

Qy   1801 GATCGCTTTAAAACACTCAGGAGGATCCTTGCGGCCAAAATCACCGACACTCGTCCCAC 1860
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1801 GATCGCTTTAAAACACTCAGGAGGATCCTTGCGGCCAAAATCACCGACACTCGTCCCAC 1860

Qy   1861 CCCAGAATCCCTTCAGCGTGTTGAAGAGGAAACCGCAGCCCGGGTACCG 1909
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Db   1861 CCCAGAATCCCTTCAGCGTGTTGAAGAGGAAACCGCAGCCCGGGTACCG 1909


RESULT 5
US-09-951-535-3
; Sequence 3, Application US/09951535
; Publication No. US2003004980A1
; GENERAL INFORMATION:
;  APPLICANT: ZIEGLER, PETRA
;  APPLICANT: EGGELING, LOTHAR
;  APPLICANT: SAHM, HERMANN
;  APPLICANT: THIERBACH, GEORG
;  TITLE OF INVENTION: NEW NUCLEOTIDE SEQUENCES CODING FOR THE THRE GENE AND
;  TITLE OF INVENTION: PROCESS FOR THE ENZYMATIC PRODUCTION OF L-THREONINE
;  TITLE OF INVENTION: USING CORYNEFORM BACTERIA
;  FILE REFERENCE: 21123/282415/MAS
;  CURRENT APPLICATION NUMBER: US/09/951,535
;  CURRENT FILING DATE: 2001-09-14
;  PRIOR APPLICATION NUMBER: 09/431,099
;  PRIOR FILING DATE: 1999-11-01
;  PRIOR APPLICATION NUMBER: DE 199 41 478.5
;  PRIOR FILING DATE: 1999-09-01
;  NUMBER OF SEQ ID NOS: 10
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
;  LENGTH: 1909
;  TYPE: DNA
;  ORGANISM: Corynebacterium glutamicum
;  FEATURE:
;  NAME/KEY: CDS
;  LOCATION: (280)..(1746)
;  OTHER INFORMATION: thrE-Gen
US-09-951-535-3

  Query Match          100.0%;  Score 1909;  DB 10;  Length 1909;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches 1909;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

Qy      1 AGCTTGCATGCCAGGTCGACTCTAGAGGATCCCCCCCTTGACCTGGTGTTATTGA 60
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Db      1 AGCTTGCATGCCAGGTCGACTCTAGAGGATCCCCCCCTTGACCTGGTGTTATTGA 60

Qy     61 GCTGGAGAAGAGACTTGAACTCTCAACCTACCAAGTGCGTGGCGCTGCCAATTG 120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 GCTGGAGAAGAGACTTGAACTCTCAACCTACCAAGTGCGTGGCGCTGCCAATTG 120

Qy    121 CGCCACTCCAGCCACCGAGATGCTGATGATCAACTACGAATACGTATCCTAGCGTAT 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 CGCCACTCCAGCCACCGAGATGCTGATGATCAACTACGAATACGTATCCTAGCGTAT 180

Qy    181 GTGTACATCACAATGGAATTCGGGCGTAGAGTATCGTGACCGTGCATAAACGACCTG 240
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Db    181 GTGTACATCACAATGGAATTCGGGCGTAGAGTATCGTGACCGTGCATAAACGACCTG 240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Qy    241 TGATTGGACTCTTTCCTTGCAAAATGTTTTCCAGCGGATGTGAGTTTGCGACCCTT 300
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 TGATTGGACTCTTTCCTTGCAAAATGTTTTCCAGCGGATGTGAGTTTGCGACCCTT 300

Qy    301 CGTGGCCGCATTCAACAGTTGACGCTGCAAAAGCCGCACCTCCGCCATCGCCACTAGCC 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 CGTGGCCGCATTCAACAGTTGACGCTGCAAAAGCCGCACCTCCGCCATCGCCACTAGCC 360

Qy    361 CCGATTGATCTCACTGACCATAGTCAAGTGGCCGGTGTGATGATGGCTGCGAGAATT 420
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 CCGATTGATCTCACTGACCATAGTCAAGTGGCCGGTGTGATGATGGCTGCGAGAATT 420

Qy    421 GGCGATATTTGCTTTCTTCAGGTACGTCAAATAGTGACACCAAGGTACAAGTTCGAGCA 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 GGCGATATTTTGCTTTCTTCAGGTACGTCAAATAGTGACACCAAGGTACAAGTTCGAGCA 480

Qy    481 GTGACCTCTGCGTACGGTTTGTACTACACGACGTGGATATCACGTTGAATACGATCACC 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 GTGACCTCTGCGTACGGTTTGTACTACACGACGTGGATATCACGTTGAATACGATCACC 540

Qy    541 ATCTTCACCAACATCGGTGTGGAGGAAGATGCCGGTCAACGTGTTCATCGTGTTGTAGGC 600
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 ATCTTCACCAACATCGGTGTGGAGGAAGATGCCGGTCAACGTGTTCATCGTGTTGTAGGC 600

Qy    601 AAGTTGGACACCAACTTCTCCAAACTGTCTGAGGTTGACCGTTGGAGCAATCCCCT 660
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 AAGTTGGACACCAACTTCTCCAAACTGTCTGAGGTTGACCGTTGGAGCAATCCCCT 660

Qy    661 GCTGGTGCGACCCGCCTGAGGTTGCCGAGAAATCTGGACGAGTTGGAGCAATCCCCT 720
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 GCTGGTGCGACCCGCCTGAGGTTGCCGAGAAATCTGGACGAGTTGGAGCAATCCCCT 720

Qy    721 GCGTCTTATGGTTTCCCTGCGTTGCGTTGCTGGCGGCAATGATGGGTGGTGCTGTGTGCT 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 GCGTCTTATGGTTTCCCTGCGTTGCGTTGCTGGCGGCAATGATGGGTGGTGCTGTGTGCT 780

Qy    781 GTGCTGTTGGGTGGTGGATGGCAGGTTCCCTAATTGCTTTTATTACCGCGTTCACGATC 840
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 GTGCTGTTGGGTGGTGGATGGCAGGTTCCCTAATTGCTTTTATTACCGCGTTCACGATC 840

Qy    841 ATTGCCACGACGTCATTTTGGGAAAGAAGGGTTTGCCTACTTTCTTCCAAAATGTTGTT 900
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 ATTGCCACGACGTCATTTTGGGAAAGAAGGGTTTGCCTACTTTCTTCCAAAATGTTGTT 900

Qy    901 GGTGGTTTTATTGCCACGCTGCCTGCGCTGATTGCTTATTCTTGGCGTTGCAATTGGT 960
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 GGTGGTTTTATTGCCACGCTGCCTGCGCTGATTGCTTATTCTTGGCGTTGCAATTGGT 960

Qy    961 CTTGAGATCAAACCGAGCCAGCAGATCATCGCATCTGGAATTGTGTGCTTGGCAGGTTTG 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961 CTTGAGATCAAACCGAGCCAGCAGATCATCGCATCTGGAATTGTGTGCTTGGCAGGTTTG 1020

Qy   1021 ACACTCGGTGCAATCTCTGCAGGACGGCCATCACGGCGCTCCGGTGCGCTGCACGA 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 ACACTCGGTGCAATCTCTGCAGGACGGCCATCACGGCGCTCCGGTGCGCTGCACGA 1080

Qy   1081 TTTTTCGAAACACTCCTGTTTACCGGGGCATTGGTGCTGGCGGGTTGGGCATTCAG 1140
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 TTTTTCGAAACACTCCTGTTTACCGGGGCATTGGTGCTGGCGGGTTGGGCATTCAG 1140

Qy   1141 CTTTCTGAAATCTTGACGTCATGTTCGATGTTGCTGCCATGAGTCCGCTGCACCTAATTAT 1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141 CTTTCTGAAATCTTGACGTCATGTTCGATGTTGCTGCCATGAGTCCGCTGCACCTAATTAT 1200

Qy   1201 TCGTCTACATTGCCCCGCGATTATCGCTGGTGGTGCGGCCTTCCAGTGGGGT 1260
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1201 TCGTCTACATTGCCCCGCGATTATCGCTGGTGGTGCGGCCTTCCAGTGGGGT 1260

Qy   1261 TGTTACCGGGAGTGGTCTCGGTGATTATTGCGGGGGCTTACTGCTGATGGGGTTCTCGCG 1320
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy      1 AGCTTGCATGCCTGCGACTCTAGAGGATCCCCCCCTTTGACCTGGTGTTATTGA 60

Db        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     61 GCTGGAGAGAGACTTGAACTCTCAACCTACCATTACAAGTGCGGTTGCGCTGCCAATTG 120
Db     61 GCTGGAGAGAGACTTGAACTCTCAACCTACCATTACAAGTGCGGTTGCGCTGCCAATTG 120

Db        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    121 CGCCACTTCCAGCACCGCAGATGCTGATGATCAACAACTACGAATACGTATCTTAGCGTAT 180
Db    121 CGCCACTTCCAGCACCGCAGATGCTGATGATCAACAACTACGAATACGTATCTTAGCGTAT 180

Db        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    181 GTGTACATCACAATGGAATTCGGGGCTCAGAGTATCTGTGAACCGTGAACCGTGCATAAACGACCTG 240
Db    181 GTGTACATCACAATGGAATTCGGGGCTCAGAGTATCTGTGAACCGTGAACCGTGCATAAACGACCTG 240

Db        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    241 TGATTGGACTCTTTCCTTGCAAAATGTTTTCCAGCCGATGTTGAGTTTGCGACCCTT 300
Db    241 TGATTGGACTCTTTCCTTGCAAAATGTTTTCCAGCCGATGTTGAGTTTGCGACCCTT 300

Db        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    301 CGTGGCCGCATTCAACAGTTGACGCTGCAAAGCCGACACCTGCACCTGCCACTAGCC 360
Db    301 CGTGGCCGCATTCAACAGTTGACGCTGCAAAGCCGACACCTGCACCTGCCACTAGCC 360

Db        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    361 CCGATTGATCTCACTGACCATAGTCAAGTGGCCGGTGTGATGAATTGGCTGCGAGAATT 420
Db    361 CCGATTGATCTCACTGACCATAGTCAAGTGGCCGGTGTGATGAATTGGCTGCGAGAATT 420

Db        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    421 GGCGATATTTGCTTCTTCAGGTACGTCAAATAGTGACACCAAGGTACAAGTTCGAGCA 480
Db    421 GGCGATATTTGCTTCTTCAGGTACGTCAAATAGTGACACCAAGGTACAAGTTCGAGCA 480

Db        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    481 GTGACCTCTGCGTACGGTTTGTACTACACGCACGTGGATATCACGTTGAATACGATCACC 540
Db    481 GTGACCTCTGCGTACGGTTTGTACTACACGCACGTGGATATCACGTTGAATACGATCACC 540

Db        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    541 ATCTTCACCAACATCGGTGTGGAGAGAAGATGCCGGTCAACGTGTTTCATGTGTAGGC 600
Db    541 ATCTTCACCAACATCGGTGTGGAGAGAAGATGCCGGTCAACGTGTTTCATGTGTAGGC 600

Db        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    601 AAGTTGGACACCAACTTCTCCAAACTCTCGAGGTTGACCGTTGATCCGTTCCATTCAG 660
Db    601 AAGTTGGACACCAACTTCTCCAAACTCTCGAGGTTGACCGTTGATCCGTTCCATTCAG 660

Db        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    661 GCTGGTGCGACACCCGCCTGAGGTTGCCGAGGAAATCCTGGAGCAATCCCT 720
Db    661 GCTGGTGCGACACCCGCCTGAGGTTGCCGAGGAAATCCTGGAGCAATCCCT 720

Db        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    721 GGGTCTTATGGTTTCCCTGTTGCTTGCGTTGGCTGGCCAATGATGGGGTGCTGTTGCT 780
Db    721 GGGTCTTATGGTTTCCCTGTTGCTTGCGTTGGCTGGCCAATGATGGGGTGCTGTTGCT 780

Db        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    781 GTGCTGTTGGGTGGTGGATGGCAGGTTCCCTAATTGCTTTTATTACCCGTTCACGATC 840
Db    781 GTGCTGTTGGGTGGTGGATGGCAGGTTCCCTAATTGCTTTTATTACCCGTTCACGATC 840

Db        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    841 AATTGCCACGACGTCATTTTTGGGAAAGAAAGGGTTTGCCTACTTTCTTCTTGGCCTT 900
Db    841 AATTGCCACGACGTCATTTTTGGGAAAGAAAGGGTTTGCCTACTTTCTTCTTGGCCTT 900

Db        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    901 GGTGGTTTATTGCCACGCTGCCACGCTGCCGATCGATCGATTGCTTATTCTTTGGCAATTTGT 960
Db    901 GGTGGTTTATTGCCACGCTGCCACGCTGCCGATCGATCGATTGCTTATTCTTTGGCAATTTGT 960

Db        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    961 CTTGAGATCAAACCGAGCCAGATCATCCGCATCCGGAATTGTGTCGTGGCAGGTTTG 1020
Db    961 CTTGAGATCAAACCGAGCCAGATCATCCGCATCCGGAATTGTGTCGTGGCAGGTTTG 1020

Db        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1021 ACACTCGGTGCAATCTTCTGCAGGACGGCATCACGGGCGCTCCGGTGACAGCAAGTGCACGA 1080
Db   1021 ACACTCGGTGCAATCTTCTGCAGGACGGCATCACGGGCGCTCCGGTGACAGCAAGTGCACGA 1080

Db        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1081 TTTTTCGAAACACTCCTGTTTACCGGGGATCCCCCCTTTGACCTGGTGTTATTGA 1140
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Db   1261 TGTTACCGGAGTGGTCCTCGTGATTATTGCGGGCTTACTGCGCTGATGGTTCTGCGG 1320

Db        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1321 TTTTATTACCTCTTCGTGTTTATTGTAGGCCCCGTCTCTGCCGATTGCTGCGAACA 1380
Db   1321 TTTTATTACCTCTTCGTGTTTATTGTAGGCCCCGTCTCTGCCGATTGCTGCGAACA 1380

Db        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1381 GCAGTTGGTTCACTGGTGGTTGCTTGCCCCTGAATTCTTGATTCTTCCACCGTTGATTGTG 1440
Db   1381 GCAGTTGGTTCACTGGTGGTTGCTTGCCCCTGAATTCTTGATTCTTCCACCGTTGATTGTG 1440

Db        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1441 GCGATTGCCGGCATCACACAACGCTTCCAGGTCTAGCAATTACCGCGGAATGTACGCC 1500
Db   1441 GCGATTGCCGGCATCACACAACGCTTCCAGGTCTAGCAATTACCGCGGAATGTACGCC 1500

Db        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1501 ACCCTGAAATGAATCAAACACTCATGGGGTTCACCAACATTGGCGGTTGCTTTAGCCACTGCT 1560
Db   1501 ACCCTGAAATGAATCAAACACTCATGGGGTTCACCAACATTGGCGGTTGCTTTAGCCACTGCT 1560

Db        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1561 TCATCACTTGCCGCGTGGTGTTTGGGTGAGTGGATTGCCCGGAGGCTACGTCGTCCA 1620
Db   1561 TCATCACTTGCCGCGTGGTGTTTGGGTGAGTGGATTGCCCGGAGGCTACGTCGTCCA 1620

Db        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1621 CCACGCTTCAACCCATACCGTGCATTACCAAGGCGAATGAGTTCTCCTTCCAGGAGGAA 1680
Db   1621 CCACGCTTCAACCCATACCGTGCATTACCAAGGCGAATGAGTTCTCCTTCCAGGAGGAA 1680

Db        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1681 GCTGAGCAGAATCAGGCGCCGGCAGAGAAAACGTCCAAAGACTAATCAGAGATTCGGTAAT 1740
Db   1681 GCTGAGCAGAATCAGGCGCCGGCAGAGAAAACGTCCAAAGACTAATCAGAGATTCGGTAAT 1740

Db        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1741 AAAAGGTAAAAATCAACCTGCTTAGGCGTCTTTCGCTTAAATAGCGGTAGAATATCGGGTC 1800
Db   1741 AAAAGGTAAAAATCAACCTGCTTAGGCGTCTTTCGCTTAAATAGCGGTAGAATATCGGGTC 1800

Db        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1801 GATCGCGTTTTAAACACTCAGGAGGATCCTTGCGGCGGCCAAAATCACGGACACTCGTCCCAC 1860
Db   1801 GATCGCGTTTTAAACACTCAGGAGGATCCTTGCGGCGGCCAAAATCACGGACACTCGTCCCAC 1860

Db        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1861 CCCAGAAATCCCTGTTGAAGGAGAAACCGCAGCCGGGGTACCG 1909
Db   1861 CCCAGAAATCCCTGTTGAAGGAGAAACCGCAGCCGGGGTACCG 1909
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Query Match   100.0%;   Score 1909;   DB 17;   Length 1909;
Best Local Similarity   100.0%;   Pred. No. 0;
Matches 1909;   Conservative 0;   Mismatches 0;   Indels 0;   Gaps 0;

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Qy      1 AGCTTGCATGCCTGCGACTCTAGAGGATCCCCCCCTTTGACCTGGTGTTATTGA 60
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; CURRENT FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: JP 99/377484
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: JP 00/159162
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: JP 00/280988
; PRIOR FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 7059
; SOFTWARE: PatentIn ver. 3.0
; SEQ ID NO 1
; LENGTH: 3309400;
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
US-09-738-626-1

Query Match        97.7%;  Score 1865.4;  DB 9;  Length 3309400;
Best Local Similarity 99.9%;  Pred. No. 0;
Matches 1866;  Conservative 0;  Mismatches 0;  Indels 1;  Gaps 0;

Qy        38 CCCCTTTGACCGTGGTGTTATTGAGCTGGAGAAGAGACTTGAACTCTCAACCTACCGCATTA       97
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2790740 CCCCTTTGACCGTGGTGTTATTGAGCTGGAGAAGAGACTTGAACTCTCAACCTACCGCATTA  2790799

Qy        98 CAAGTGCGTTGCGTTGCCAATTGGCCACTCCAGCACCGCAGATGCTGATGATCAACAAC      157
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2790800 CAAGTGCGTTGCGTTGCCAATTGGCCACTCCAGCACCGCAGATGCTGATGATCAACAAC   2790859

Qy       158 TACGAATACGTATCTTAGCGTATGTGTACATCACAATGGAATTCGGGGCTAGAGTATCTG     217
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2790860 TACGAATACGTATCTTAGCGTATGTGTACATCACAATGGAATTCGGGGCTAGAGTATCTG  2790919

Qy       218 GTGAACCGTGCATAAACGACCTGTGATTGGACTCTTTTTCCTTGCAAAATGTTTTCCAGC     277
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2790920 GTGAACCGTGCATAAACGACCTGTGATTGGACTCTTTTTCCTTGCAAAATGTTTTCCAGC  2790979

Qy       278 GGATGGTTGAGTTTTGCGACCCCTTCGTGGCGCGCAATTCAACAGTTGACGCTGCAAAAGCCG  337
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2790980 GGATGGTTGAGTTTTGCGACCCCTTCGTGGCGCGCAATTCAACAGTTGACGCTGCAAAAGCCG 2791039

Qy       338 CACCTTCCGCCATCGCCACTAGCCCCGATTGATCTCACTGACCATAGTCAAGTGGCCGGTG    397
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2791040 CACCTTCCGCCATCGCCACTAGCCCCGATTGATCTCACTGACCATAGTCAAGTGGCCGGTG 2791099

Qy       398 TGATGAATTTGGCTGCGAGAATTGGCGATATTTTGCTTTCTTCAGGTACGTCAAATAGTG    457
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2791100 TGATGAATTTGGCTGCGAGAATTGGCGATATTTTGCTTTCTTCAGGTACGTCAAATAGTG 2791159

Qy       458 ACACCAAGGTACAAGTTCGAGCAGTGACCTCGCGTACGGTTTGTACTACGCACGTGG      517
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2791160 ACACCAAGGTACAAGTTCGAGCAGTGACCTCGCGTACGGTTTGTACTACGCACGTGG   2791219

Qy       518 ATATCACGTTGAATACGTTCAGCAGTTGACCTTCACCAACATCGTGTGAGAGAAGATGCCGG  577
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2791220 ATATCACGTTGAATACGTTCAGCAGTTGACCTTCACCAACATCGTGTGAGAGAAGATGCCGG 2791279

Qy       578 TCAACGTGTTCATGTTGTAGGCAAGTTGGACACCACCAACTTGAGGGTTG            637
             ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2791280 TCAACGTGTTCATGTTGTAGGCAAGTTGGACACCACCAACTTGAGGGTTG         2791339

Qy       638 ACCGGTTGATCCGTTCCATTCAGGGCTGGTGCGAACCCCGCCTGAGGGTTGCCGAGAAAATCC  697
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2791340 ACCGGTTGATCCGTTCCATTCAGGGCTGGTGCGAACCCCGCCTGAGGGTTGCCGAGAAAATCC 2791399

Qy       698 TGGACGAGTTGGAGCAATCCCCGGTCTTATGGTTGCGTTGGCGTTGGCTGGG          757
             |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2791400 TGGACGAGTTGGAGCAATCCCCGGTCTTATGGTTGCGTTGGCGTTGGCTGGG       2791459

Qy       758 CAATGATGGGTGGTGTGTTGCTGGGTGGTGGTGATGGGATGGGATGGG              817
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Db   2791460 CAATGATGGGTGGTGTGTTGCTGGGTGGTGGTGATGGGATGGGATGGG           2791519

Qy       818 CTTTTATTACCGGTTCACGATCATTGCCACGACGTCATTTTTGGGAAGAAGAGGGTTTGC   877
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Db      1081 TTTTCGAAACACTCCTGTGTTTACCGGCGGCATTGTTGCTGGCGTGGGTTTGGGCATTCAG 1140
Qy      1141 CTTTCTGAAATCTTGCATGTCATGTGTTGCTTGCCTGCCATGGAGTCGCGTGCGCAGCACCTAATTAT 1200
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1141 CTTTCTGAAATCTTGCATGTCATGTGTTGCTTGCCTGCCATGGAGTCGCAGCACCTAATTAT 1200

Qy      1201 TCGTCTACATTGCCCGCATTATCGCTGGTGGCGTCACCGCAGCGGCCTTCGCAGTGGGT 1260
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1201 TCGTCTACATTGCCCGCATTATCGCTGGTGGCGTCACCGCAGCGGCCTTCGCAGTGGGT 1260

Qy      1261 TGTTACGCGGAGTGGTGTCCTCGGTGATTATTGCGGGCTTACTGCGGCTGATGGGTTCTCGCG 1320
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1261 TGTTACGCGGAGTGGTGTCCTCGGTGATTATTGCGGGCTTACTGCGGCTGATGGGTTCTGCG 1320

Qy      1321 TTTTATTACCTTCTTCGTTGTGTTATTAGGGCCCGTCTCTGCCGCTGCGATTGCTGCAACA 1380
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1321 TTTTATTACCTTCTTCGTTGTGTTATTAGGGCCCGTCTCTGCCGCTGCGATTGCTGCAACA 1380

Qy      1381 GCAGTGGTTTCACTGGTGGTTGCTGCGTTGCTTGCTTCACCGTTGATTGTG 1440
             ||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1381 GCAGTGGTTTCACTGGTGGTTGCTGCGTTGCTTGCTTCACCGTTGATTGTG 1440

Qy      1441 GCGAATGCCGCGCATCACACAAATGCTTCAGGTCTCAGCAATTTACCGCGGAATGTACGCC 1500
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1441 GCGAATGCCGCGCATCACACAAATGCTTCAGGTCTCAGCAATTTACCGCGGAATGTACGCC 1500

Qy      1501 ACCCTGAATGATCAAACACTCATGGGGTTCACCAACACATTGCGGTTGCTTTAGCCACTGCT 1560
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1501 ACCCTGAATGATCAAACACTCATGGGGTTCACCAACACATTGCGGTTGCTTTAGCCACTGCT 1560

Qy      1561 TCATCACTTGCCGCGTCTGGCGTGTTTTGGGGTGAGTGGATTGCCCGAGGCTACGTCGTCCA 1620
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1561 TCATCACTTGCCGCGTCTGGCGTGTTTTGGGGTGAGTGGATTGCCCGAGGCTACGTCGTCCA 1620

Qy      1621 CCACGCTTCAACCCATACCGTGCATTTACCAAGGCGAATGAGTTCTCCTTCCAGGAGGAA 1680
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1621 CCACGCTTCAACCCATACCGTGCATTTACCAAGGCGAATGAGTTCTCCTTCCAGGAGGAA 1680

Qy      1681 GCTGAGCAGAATCAGCGCCGGCAGCGCCGGCAGAGAAAACGTCCAAAGACTAATCAGAGATTCGGTAAT 1740
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1681 GCTGAGCAGAATCAGCGCCGGCAGCGCCGGCAGAGAAAACGTCCAAAGACTAATCAGAGATTCGGTAAT 1740

Qy      1741 AAAAGTAAAAATCAACCTGCTTAGCGTCTTTCGCTTAAATAGCGTAGAATATCGGGTC 1800
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1741 AAAAGTAAAAATCAACCTGCTTAGCGTCTTTCGCTTAAATAGCGTAGAATATCGGGTC 1800

Qy      1801 GATCGCTTTTAAAACACTCAGGAGGATCCTTGCCGGCCAAAAATCACGGACACTCGTCCCAC 1860
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1801 GATCGCTTTTAAAACACTCAGGAGGATCCTTGCCGGCCAAAAATCACGGACACTCGTCCCAC 1860

Qy      1861 CCCAGAATCCCTTCACGCTGTTGAAGAGGAAACCGCAGCCGGGGTACCG 1909
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Db      1861 CCCAGAATCCCTTCACGCTGTTGAAGAGGAAACCGCAGCCGGGGTACCG 1909
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RESULT 7
US-09-738-626-1
; Sequence 1, Application US/09738626
; Publication No. US20020197605A1
; GENERAL INFORMATION:
; APPLICANT: NAKAGAWA, SATOSHI
; APPLICANT: MIZOGUCHI, HIROSHI
; APPLICANT: ANDO, SEIKO
; APPLICANT: HAYASHI, MIKIRO
; APPLICANT: OCHIAI, KEIKO
; APPLICANT: YOKOI, HARUHIKO
; APPLICANT: TATEISHI, NAOKO
; APPLICANT: SENOH, AKIHIRO
; APPLICANT: IKEDA, MASATO
; APPLICANT: OZAKI, AKIO
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-125
; CURRENT APPLICATION NUMBER: US/09/738,626
```

RESULT 8

US-09-951-536-1

; Sequence 1, Application US/09951536
; Patent No. US2002010737B8A1
; GENERAL INFORMATION:
; APPLICANT: ZIEGLER, PETRA
; APPLICANT: EGGELING, LOTHAR
; APPLICANT: SAHM, HERMANN
; APPLICANT: THIERBACH, GEORG
; TITLE OF INVENTION: NEW NUCLEOTIDE SEQUENCES CODING FOR THE THRE GENE AND
; TITLE OF INVENTION: PROCESS FOR THE ENZYMATIC PRODUCTION OF L-THREONINE
; TITLE OF INVENTION: USING CORYNEFORM BACTERIA
; FILE REFERENCE: 21123/282414/MAS
; CURRENT APPLICATION NUMBER: US/09/951,536
; CURRENT FILING DATE: 2001-09-14
; PRIOR APPLICATION NUMBER: 09/431,099
; PRIOR FILING DATE: 1999-11-01
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 2817
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (398)..(1864)
; OTHER INFORMATION: thrB-Gen
US-09-951-536-1

Query Match   96.2%; Score 1836.6; DB 9; Length 2817;
Best Local Similarity   99.0%; Pred. No. 0;
Matches 1848; Conservative 0; Mismatches 0; Indels 19; Gaps 0;

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Qy         38 CCCCTTTGACCTGGTGTTATTGAGCTGGAGAAGAGACTTGAACTCTCAACCTACGCATTA 97
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Db        156 CCCCTTTGACCTGGTGTTATTGAGCTGGAGAAGAGACTTGAACTCTCAACCTACGCATTA 215

Qy         98 CAAGTGCGTTGCGCTGCCAATTGCCACCTCCAGCACCGCAGATGCTGATGATCAACAAC 157
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        216 CAAGTGCGTTGCGCTGCCAATTGCCACCTCCAGCACCGCAGATGCTGATGATCAACAAC 275

Qy        158 TACGAATACGTATCTTAGCGTATGTGTACATCACAATGAATTCGGGGCTAGAGTATCTG 217
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        276 TACGAATACGTATCTTAGCGTATGTGTACATCACAATGAATTCGGGGCTAGAGTATCTG 335

Qy        218 GTGAACCGTGCATAAAGACCTGTGATTGGACTCTTTTCCTTGCAAAATGTTTTCCAGC 277
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        336 GTGAACCGTGCATAAAGACCTGTGATTGGACTCTTTTCCTTGCAAAATGTTTTCCAGC 395

Qy        278 GGATGTTGAGTTTGCGACCCCTTCGTGGCCGCATTTCAACAGTTGACGCTGCAAAAGCCG 337
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        396 GGATGTTGAGTTTGCGACCCCTTCGTGGCCGCATTTCAACAGTTGACGCTGCAAAAGCCG 455

Qy        338 CACCTCCGCCATCGCCACTAGCCCCGATTGATCTCACTGACCATAGTCAAGTGCCGGTG 397
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        456 CACCTCCGCCATCGCCACTAGCCCCGATTGATCTCACTGACCATAGTCAAGTGCCGGTG 515

Qy        398 TGATGAATTGGCTGCGAGAATTGGCGATATTTGCTTTCTTCAGGTACGTCAAATAGTG 457
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Db        516 TGATGAATTGGCTGCGAGAATTGGCGATATTTGCTTTCTTCAGGTACGTCAAACAGTG 575

Qy        458 ACACCAAGTACAAGTTCGAGCAGTGACCTCTGCGGTTGTACTACACGCACGTGG 517
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Db        576 ATACCAAGGTGCAAGTTCGAGCCGTGCTATGGCCTGTACTATACGCATGTGG 635

Qy        518 ATATCACGTTGAATACGATCACCATCTTCACCAACATCGTGTGGAGAGGAAGATGCCGG 577
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        636 ATATCACGTTGAATACGATCACCATCTTCACCAACATCGGTGTGGAGAGGAAGATGCCGG 695

Qy        578 TCAACGTGTTTCATGTTGTGTAGGCAAGTTGGACACCAACTTCTCCAAACTTGCTGTGAGGTTG 637
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Db    2791520 CTTTTATTACCGCGGTTCACGATCATTGCCACGACGTCATTTTTGGGAAAGAGAAGGGTTTGC 2791579
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Qy        878 CTACTTTCTTCCAAAAATGTGTTGGTGGTGGTTATTGCCACGCTGCCTGCCATCGATTGCTT 937
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Db    2791580 CTACTTTCTTCCAAAAATGTGTTGGTGGTGGTTATTGCCACGCTGCCTGCCATCGATTGCTT 2791639

Qy        938 ATTCTTTGGCGTTGCAATTTGGTCTTGAGATCAAACCGAGCCAGATCATCGCATCTCGAA 997
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Db    2791640 ATTCTTTGGCGTTGCAATTTGGTCTTGAGATCAAACCGAGCCAGATCATCGCATCTCGGAA 2791699

Qy        998 TTGTTGTGCTGTTGGCAGGTTGGACACTCGTGCGAGGACACGGCATCACGGGCG 1057
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Db    2791700 TTGTTGTGCTGTTGGCAGGTTGGACACTCGTGCGAGGACACGGCATCACGGGCG 2791759

Qy       1058 CTCCGGTGACAGCAAGTGCACGATTTTGAAACACTCCGTTACCGCGCGGCATTGTTG 1117
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Db    2791760 CTCCGGTGACAGCAAGTGCACGATTTTGAAACACTCCGTTACCGCGCGGCATTGTTG 2791819

Qy       1118 CTGGCGTGGGTTTGGGCATTCAGCTTTCTGAAATCTTCATGTCATGTGCCTGCCATGG 1177
              |||||||||||||||||||||||||||||||||||||||||||||
Db    2791820 CTGGCGTGGGTTTGGGCATTCAGCTTTCTGAAATCTTCATGTCATGTGCCTGCCATGG 2791879

Qy       1178 AGTCCCGCTGCAGCACCTAATTATTCGTCTACATTCGCCCGCATTATCGTCGTGTGGCGTCA 1237
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Db    2791880 AGTCCCGCTGCAGCACCTAATTATTCGTCTACATTCGCCCGCATTATCGTCGTGTGGCGTCA 2791939

Qy       1238 CCGCAGCGGCCTTCGACAGTGGGTTGTACGGTGGTCCTCGGTGATTATTGCGGGGC 1297
              |||||||||||||||||||||||||||||||||||||||||||||
Db    2791940 CCGCAGCGGCCTTCGACAGTGGGTTGTACGGTGGTCCTCGGTGATTATTGCGGGGC 2791999

Qy       1298 TTACTGCGCTGATGGGTTCTCGCGTTTATTACCTCTTCGTTGTTTATTTAGGCCCCCGTCT 1357
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Db    2792000 TTACTGCGCTGATGGGTTCTCGCGTTTATTACCTCTTCGTTGTTTATTTAGGCCCCCGTCT 2792059

Qy       1358 CTGCCGCTGCGATTGCTGCAACAGCAGTTGGTTCACTGGTGTTTGCTTGCCCGTCGAT 1417
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Db    2792060 CTGCCGCTGCGATTGCTGCAACAGCAGTTGGTTCACTGGTGTTTGCTTGCCCGTCGAT 2792119

Qy       1418 TCTTGATTCCACCGTTGATTGTGGCGATTGCCGGCGCATCACACACCAATGCTTCCAGGTCTAG 1477
              |||||||||||||||||||||||||||||||||||||||||||||
Db    2792120 TCTTGATTCCACCGTTGATTGTGGCGATTGCCGGCGCATCACACACCAATGCTTCCAGGTCTAG 2792179

Qy       1478 CAATTTACCGCGGAATGTACGCCACCTCACCCTGAATGATCAAACACTCATGGGTTTCACCAACA 1537
              |||||||||||||||||||||||||||||||||||||||||||||
Db    2792180 CAATTTACCGCGGAATGTACGCCACCTCACCCTGAATGATCAAACACTCATGGGTTTCACCAACA 2792239

Qy       1538 TTTGCGGTTGCTTTAGCCACTGCTTCATCACTTGCCCGCTGGCCGTGGTTTGGGTGAGTGGA 1597
              |||||||||||||||||||||||||||||||||||||||||||||
Db    2792240 TTTGCGGTTGCTTTAGCCACTGCTTCATCACTTGCCCGCTGGCCGTGGTTTGGGTGAGTGGA 2792299

Qy       1598 TTGCCCGCAGGCTACGTCGTCGTCATCACACGCTTCAACCACCGTGCATTTACCAAGGCGA 1657
              |||||||||||||||||||||||||||||||||||||||||||||
Db    2792300 TTGCCCGCAGGCTACGTCGTCGTCATCACACGCTTCAACCACCGTGCATTTACCAAGGCGA 2792359

Qy       1658 ATGAGTTCTCCTTCCAGGAGGAAGCTGAGCAGAATCAGCGCGCCGGCAGAGAAAACGTCCAA 1717
              |||||||||||||||||||||||||||||||||||||||||||||
Db    2792360 ATGAGTTCTCCTTCCAGGAGGAAGCTGAGCAGAATCAGCGCGCCGGCAGAGAAAACGTCCAA 2792419

Qy       1718 AGACTAATCAGAGATTCGGTAATAAAGGTAAAAATCAACCTGCTTAGGCGTCTTTCGCT 1777
              |||||||||||||||||||||||||||||||||||||||||||||
Db    2792420 AGACTAATCAGAGATTCGGTAATAAAGGTAAAAATCAACCTGCTTAGGCGTCTTTCGCT 2792479

Qy       1778 TAAATAGCTAGAATATCGGGTCGATCGCTTTAAACACTCAGGAGGATCCTTGCCGGCC 1837
              |||||||||||||||||||||||||||||||||||||||||||||
Db    2792480 TAAATAGCTAGAATATCGGGTCGATCGCTTTAAACACTCAGGAGGATCCTTGCCGGCC 2792539

Qy       1838 AAAATCACGGACACTCGTCCCACCCCAGAATCCCTTCACGCTGTTGAAGAGGAAACCGCA 1897
              |||||||||||||||||||||||||||||||||||||||||||||
Db    2792540 AAAATCACGGACACTCGTCCCACCCCAGAATCCCTTCACGCTGTTGAAGAGGAAACCGCA 2792599

Qy       1898 GCCGGGG 1904
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Db    2792600 GCCGGGTG 2792606
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Db   696 TCAACGTGTTGTTCATGTTGTGGGCAAGTTGGACACCAACTTCTCCAAACTGTCTGAGGTTG 755

Qy   638 ACCGTTTGATCCGTTCCATTCAGGCTGGTGCTGGCTGCCGAGAAAATCC 697
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Db   756 ACCGTTTGATCCGTTCCATTCAGGCTGGTGCTGGCTGCCGAGAAAATTC 815

Qy   698 TGGACGAGTTGGAGCAATCGCCGCGTCCTATGTGTTCCCTGTCGTTGCGTTGCTGGCTGGG 757
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Db   816 TGGACGAGTTGGAGCAATCGCCGCGTCCTATGTGTTCCCTGTCGTTGCGTTGCTGGCTGGG 875

Qy   758 CAATGATGGGTGGTGCGGCGCTGCGTGTCGTGTCGTGGGTGGTGTGGGGTGTTCCCTAATTG 817
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   876 CAATGATGGGTGGCGGCGCTGCGTGTCGTGTCGTGGGTGGTGTGGGGTGTTCCCTAATTG 935

Qy   818 CTTTTATTACCGCGTTCACGATCATTGCCACGACGTCATTTTGGGAAAGAGGGTTTGC 877
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   936 CTTTTATTACCGCGTTCACGATCATTGCCACGCGTCATTTTTGGGAAAGAGGGTTTGC 995

Qy   878 CTACTTTCTTCCAAAATGTTGTTGGTGGTTTATTGCCACGCTGCCTGCGATTCGTTGCTT 937
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Db   996 CTACTTTCTTCCAAAATGTTGTTGGTGGTTTATTGCCACGCTGCCTGCGATTCGTTGCTT 1055

Qy   938 ATTCTTTGGCGTTGCAATTTGGGTCTTGAGATCAAAACCGAGCCAGATCATCGCATCTGGAA 997
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Db 1056 ATTCTTTGGCGTTGCAATTTGGGTCTTGAGATCAAAACCGAGCCAGATCATCGCATCTGGAA 1115

Qy   998 TTGTTGTCGTGTTGGCAGGTTGGCACGATTTTCGAAACACTCTCGTTTACCGGCGGCATCACGGGCG 1057
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1116 TTGTTGTCGTGTTGGCAGGTTGGCACGATTTTTTGAAACACTCTCGTTTACCGGCGGCATCACGGGCG 1175

Qy 1058 CTCCGGTGACAGCAAGTGCACGATTTTCGAAACACTCTCGTTTACCGGCGGCATTGTTG 1117
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Db 1176 CTCCGGTGACAGCAAGTGCACGATTTTTTGAAACACTCTCGTTTACCGGCGGCATTGTTG 1235

Qy 1118 CTGGGCTGGGGTTTGGGCATTCAGCTTTCTGAAAATCTTGCATGTCATGTTGCTGCTGCCATGG 1177
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Db 1236 CTGGGCTGGGGTTTGGGCATTCAGCTTTCTGAAAATCTTGCATGTCATGTTGCTGCTGCCATGG 1295

Qy 1178 AGTCCGGCTGCAGCACCTAATTATTCGTCTACATTCGCCCGCCATTATTCGCTGGTGCGTCA 1237
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1296 AGTCCGGCTGCAGCACCTAATTATTCGTCTACATTCGCCCGCCATTATTCGGTGGCGTCA 1355

Qy 1238 CCGCAGGGGCCTTCGACAGTGGTGTTACGCGGAGTTGCTCCTCGGTGATTATTGCGGGGGC 1297
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Db 1356 CCGCAGGGGCCTTCGACAGTGGTGTTACGCGGAGTTGCTCCTCGGTGATTATTGCGGGGGC 1415

Qy 1298 TTACTGCGCTGATGGGTTCTGCGTTTATTACCTCTCTTGTTGTTTATTTAGGCCCCGTCT 1357
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Db 1416 TTACTGCGCTGATGGGTTCTGCGTTTATTACCTCTCTTGTTGTTTATTTAGGCCCCGTCT 1475

Qy 1358 CTGCCCGGCTGCGAACAGCAGTGGTTCTGCAACAGCAGTTGGTTTGCTTGCTTCACTGGTTGCCCGTCGAT 1417
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Db 1476 CTGCCCGGCTGCGAACAGCAGTGGTTCTGCAACAGCAGTTGGTTTGCTTGCTTCACTGGTTGCCCGTCGAT 1535

Qy 1418 TCTTGATTCCACCGTTGATTGTGCGCATCACACCAATGCTTCAACCACCATCACTTCTTCCAGGTCTAG 1477
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1536 TCTTGATTCCACCGTTGATTGTGCGCATCACACCAATGCTTCAACCACCATCACTTCTTCCAGGTCTAG 1595

Qy 1478 CAATTTACCGCCGGAATGTACGGCCACCCTGAATGATCAAACACTCATGGGTTTCACCAACA 1537
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1596 CAATTTACCGCCGGAATGTACGGCCACCCTGAATGATCAAACACTCATGGGTTTCACCAACA 1655

Qy 1538 TTGCGGTTGCTTTAGCCACTGCTTCATCACTTGCCGCGTGGCGTGGTTTGGGTGAGTGGA 1597
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1656 TTGCGGTTGCTTTAGCCACTGCTTCATCACTTGCCGCGTGGCGTGGTTTGGGTGAGTGGA 1715

Qy 1598 TTGCCCAGGCTACGTCGTCGTCACCACCGCGTTCAACCGTGCATTTACCAAGGCGA 1657
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Db 1716 TTGCCCAGGCTACGTCGTCGTCACCACCGCGTTCAACCGTGCATTTACCAAGGCGA 1775

Qy 1658 ATGAGTTCCTTCCAGGAGGAGCTGAGCAGAATCAGGCCGCGCCGGCAGAGAAAACGTCCAA 1717
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1776 ATGAGTTCCTTCCAGGAGGAGCTGAGCAGAATCAGGCCGCGCCGGCAGAGAAAACGTCCAA 1835

Qy 1718 AGACTAATCAGAGATTCGGTAATAAAAGTAAAAATCAACCTGCTTACGGGTCTCTTCGCT 1777
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Db 1836 AGACTAATCAAAGATTCGGTAATAAAAGGTAAAAATCAACCTGCTTAGGGGTCTCTTCGCT 1895

Qy 1778 TAAATAGGCGTAGAATATCGGGTCGATGCTTTTAAACACTCAGGAGGATCCTTGCCGGCC 1837
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1896 TAAATAGGCGTAGAATATCGGGTCGATCGCTTTTAAACACTCAGGAGGATCCTTGCCGGCC 1955

Qy 1838 AAAATCACGGACACTCGTCCCCAGATACCCTTCACGCTGTTGAAGAGGAAACCGCA 1897
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1956 AAAATCACGGACACTCGTCCCCAGAATCCCTTCACGCTGTTGAAGAGGAAACCGCA 2015

Qy 1898 GCCGGGG 1904
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Db 2016 GCCGGTG 2022

RESULT 9
US-09-963-521-1
; Sequence 1, Application US/09963521
; Patent No. US20020146781A1
; GENERAL INFORMATION:
; APPLICANT: ZIEGLER, PETRA
; APPLICANT: EGGELING, LOTHAR
; APPLICANT: SAHM, HERMANN
; TITLE OF INVENTION: NEW NUCLEOTIDE SEQUENCES CODING FOR THE THRE GENE
; TITLE OF INVENTION: AND PROCESS FOR THE ENZYMATIC PRODUCTION OF
; TITLE OF INVENTION: L-THREONINE USING CORYNEFORM BACTERIA
; FILE REFERENCE: 21123/282413/MAS
; CURRENT APPLICATION NUMBER: US/09/963,521
; CURRENT FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: 09/431,099
; PRIOR FILING DATE: 1999-11-01
; PRIOR APPLICATION NUMBER: DE 199 41 478.5
; PRIOR FILING DATE: 1999-09-01
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 1
; LENGTH: 2817
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (398)..(1864)
; OTHER INFORMATION: thrE-Gen
US-09-963-521-1

Query Match   96.2%; Score 1836.6; DB 9; Length 2817;
Best Local Similarity   99.0%; Pred. No. 0;
Matches 1848; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

Qy   38 CCCCTTTGACCTGGTGTTATTGAGCTGGAGAAGAGACTTGAACTCTCAACCTACGCATTA 97
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   156 CCCCTTTGACCTGGTGTTATTGAGCTGGAGAAGAGACTTGAACTCTCAACCTACGCATTA 215

Qy   98 CAAGTGGTTGCGTGCTGCCAATTGCGCCAGTGCCACTCCAGCACCGCCAGATGCTGATGATCAACAAC 157
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Db   216 CAAGTGGTTGCGTGCTGCCAATTGCGCCAGTGCCACTCCAGCACCGCCAGATGCTGATGATCAACAAC 275

Qy   158 TACGAATACGTATCTTAGCGTATGTGTACATCACAATGGAATTCGGGGCTAGAGTATCTG 217
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Db   276 TACGAATACGTATCTTAGCGTATGTGTACATCACAATGGAATTCGGGGCTAGAGTATCTG 335

Qy   218 GTGAACCGTGCATAAACGACCTGGTTGCTTGATTGGACTCTTTCCTTGCAAAATGTTTCCAGC 277
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   336 GTGAACCGTGCATAAACGACCTGGTTGCTTGATTGGACTCTTTTCCTTGCAAAATGTTTCCAGC 395

Qy   278 GGATGTTGAGTTTTGCGACCCTTCGTGCGCCAATGCTCAACAGTTGACGCTGCAAAAGCCG 337
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Db   396 GGATGTTGAGTTTTGCGACCCTTCGTGCGCCAATGCTCAACAGTTGACGCTGCAAAAGCCG 455

Qy   338 CACCTCCGCCATCGCCACTAGCCCCGATTGATCTCACTGACCATAGTCCACCATAGTCGCCGGTG 397

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Db          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      456   CACCTCCGCCATCGCCACTAGCCCGATTGATCTCACTGACACCATAGTCAAGTTGGCCGGTG   515

Qy    398   TGATGAATTTGGCTGCGGAGAATTGGCGATATTTGCTTCTTCTTCAGGTACGTCAAATAGTG   457
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    516   TGATGAATTTGGCTGCGGAGAATTGGCGATATTTGCTTCTTCTTCAGGTACGTCAAACAGTG   575

Qy    458   ACACCAAGGTACAAGTTCGAGCAGTGACCTCTGCGTACGGTTTGTACTACACGCACGTGG    517
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    576   ATACCAAGGTGCAAGTTCGAGCGGTGACCTCTGCTATGGCCGTGTACTATACGCATGTGG    635

Qy    518   ATATCACGTTGAATACGATCACCATCTTCACCAACATCGGTCGTGGAGGAAGATGCCGG    577
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    636   ATATCACGTTGAATACGATCACCATCTTCACCAACATCGGTGTGGGAGGAAGATGCCGG    695

Qy    578   TCAACGTGTTCATGTGTGTAGGCAAGTTGGACACCAACTTCTCCAAACTGTCTGAGGTTG   637
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    696   TCAACGTGTTCATGTGTGTGGGCAAGTTGGACACCAACTTCTCCAAACTGTCTGAGGTTG   755

Qy    638   ACCGGTTTGATCCGTTCATTCAGGCTGCTGCGACCCCGCCTGAGGTTGCCGAGAAAATCC   697
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    756   ACCGGTTTGATCCGTTCATTCAGGCTGCTGCGACCCCGCCTGAGGTTGCCGAGAAAATTC   815

Qy    698   TGGACGAGTTGGAGCAATCCCTGCGTCTTATGGTTTCCCGTTGCGTTGCTGGCTTGGG   757
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    816   TGGACGAGTTGGAGCAATCGCCTGCGTCTTATGGTTTCCCGTTGCGTTGCTGGCTTGGG   875

Qy    758   CAATGATGGGTGGTGCTGTGCTGTTGTGTGCGTTCCCTAATTG   817
            |||||||||||||||||||||||||||||||||||||||||||
Db    876   CAATGATGGGTGGTGCTGTGCTGTTGTGTGCGTTTCCCTAATTG   935

Qy    818   CTTTTATTACCGGCGTTCACGATCATTGCCACGACGTCATTTTGGGAAAGAAGGGTTTGC   877
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    936   CTTTTATTACCGGCGTTCACGATCATTGCCACGACGTCATTTTGGGAAAGAAGGGGTTTGC   995

Qy    878   CTACTTTCTTCTTCCAAAATGTGTTGTGGTGGTTTATTGCCACGCGCTGCCTGCATCGATTGCTT    937
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Db    996   CTACTTTCTTCTTCCAAAATGTGTTGGTGGTTTATTGCCACGCGCTGCCTGCATCGATTGCTT   1055

Qy    938   ATTCTTTGGCGTTGCAATTTGGTCTTGAGATCAAACCGAGCCAGATCATCGGCCATCGAA    997
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Db    1056  ATTCTTTGGCGTTGCAATTTGGTCTTGAGATCAAACCGAGCCAGATCATCGGCCATCGAA   1115

Qy    998   TTGTTGTGTGCGTTGGCAGGTTTGGCAGGTTTGACACTCGTGCAATCTCTGCGAGGACACGGGCCG   1057
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Db    1116  TTGTTGTGTGCGTTGGCAGGTTTGGCAGGTTTGACACTCGTGCAATCTCTGCGAGGACACGGGCG   1175

Qy    1058  CTCCGGTGACAGCAGCAAGTGCACGATTTTTGAAACACTCCTGTTTACCGGCCATTGTTG   1117
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Db    1176  CTCCGGTGACAGCAGCAAGTGCACGATTTTTGAAACACTCCTGTTTACCGGCCATTGTTG   1235

Qy    1118  CTGGCGTGGGTTGGGCATTCAGCTTTCTGCTTTCTGAAATCTTGCATGTGCCTGCCATGG   1177
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Db    1236  CTGGCGTGGGTTGGGCATTCAGCTTTCTGCTTTCTGAAATCTTGCATGTGCCTGCCATGG   1295

Qy    1178  AGTCCGCTGCAGCACCTAATTATTCGTCTACATTCGCCCGCATTATCGCTGGTGGCGTCA   1237
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Db    1296  AGTCCGCTGCAGCACCTAATTATTCGTCTACATTCGCCCGCATTATCGCTGGTGGCGTCA   1355

Qy    1238  CCGCAGCGGCCCTTCGCAGTGGGTTGTACGCGGGAGTGGCTCCGGAGTGGTCTCCGGGGGC   1297
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Db    1356  CCGCAGCGGCCCTTCGCAGTGGGTTGTACGCGGGAGTGGCTCCGGAGTGGTCTCCGGGGGC   1415

Qy    1298  TTACTGCGCTGATGGGTTCTGCGTTTGTTATTAGGCCCCGTCT   1357
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Db    1416  TTACTGCGCTGATGGGTTCTGCGTTTGTTATTAGGCCCCGTCT   1475

Qy    1358  CTGCCGCTGCGATTGCTGCAACAGCAGTTGGTTTCACTGGTGTTTGCTTGCTTGCCCGTCGAT   1417
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1476  CTGCCGCTGCGATTGCTGCAACAGCAGTTGGTTTCACTGGTGTTTGCTTGCTTGCCCGTCGAT   1535

Qy    1418  TCTTTGATTCCACCGTTGATTGTGGCCGGATTGCCGGCATCACACACCACCAATGCTTCCAGGTCTAG   1477
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db    1536  TCTTGATTCCACCGTTGATTGTGGCCGGCATCACACACCACCAATGCTTCCAGGTCTAG   1595

Qy    1478  CAATTACCGCGGAATGTACGCCACCTGAATGATCAAACACTCACTGGGTTTCACCAACA   1537
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Db    1596  CAATTACCGCGGAATGTACGCCACCTTGAATGATCAAACACTCATGGGTTTCACCAACA   1655

Qy    1538  TTGCGGTTGCTTAGCCACTGCTTCATCACTGCTTTGGGTGTTTGGGTGTGAGTGGA   1597
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Db    1656  TTGCGGTTGCTTAGCCACTGCTTCATCACTGCTTTGGGTGTTTGGGTGTGAGTGGA   1715

Qy    1598  TTGCCCGAGGCTACGTCGTCACCACGCTTCAACCCATACCGTGCATTTACCAAGGCGA   1657
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Db    1716  TTGCCCGAGGCTACGTCGTCACCACGCTTCAACCCATACCGTGCATTTACCAAGGCGA   1775

Qy    1658  ATGAGTTCTCCTTCCAGGAGGAAGCTGAGCAGAATCAGCGCCGCCAGAGAAAACGTCCAA   1717
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1776  ATGAGTTCTCCTTCCAGGAGGAAGCTGAGCAGAATCAGCGCCGCCAGAGAAAACGTCCAA   1835

Qy    1718  AGACTAATCAGAGATTCGGTAATAAAAGGTAAAAATCAACCTGCTTCTTTCGCT   1777
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1836  AGACTAATCAAAGATTCGGTAATAAAAGGTAAAAATCAACCTGCTTCTTTCGCT   1895

Qy    1778  TAAATAGGTAGAATATCGGTGATCGTCGTTTTAAACACTCAGGAGGACGGATCCTTGCCGGCC   1837
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1896  TAAATAGGTAGAATATCGGTGATCGTCGTTTTAAACACTCAGGAGGACGGATCCTTGCCGGCC   1955

Qy    1838  AAAATCACGGACACTCGTCCCACCCCAGAATCCCTTGCACGCTGTGTTGAAGAGGAAACCGCA   1897
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Db    1956  AAAATCACGGACACTCGTCCCACCCCAGAATCCCTTCACGCTGTGTTGAAGAGGAAACCGCA   2015

Qy    1898  GCCGGGG   1904
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Db    2016  GCCGGTG   2022
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RESULT 10
US-09-834-721-1
; Sequence 1, Application US/09834721
; Patent No. US2002015555A1
; GENERAL INFORMATION:
;  APPLICANT: RIEPING, MECHTHILD
;  TITLE OF INVENTION: PROCESS FOR THE FERMENTATIVE PREPARATION OF L-THREONINE
;  FILE REFERENCE: 21123/280169/MAS
;  CURRENT APPLICATION NUMBER: US/09/834,721
;  CURRENT FILING DATE: 2001-04-16
;  PRIOR APPLICATION NUMBER: DE 100 26 494.8
;  PRIOR FILING DATE: 2000-05-27
;  PRIOR APPLICATION NUMBER: DE 101 02 823.7
;  PRIOR FILING DATE: 2001-01-23
;  NUMBER OF SEQ ID NOS: 12
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
;  LENGTH: 2817
;  TYPE: DNA
;  ORGANISM: Corynebacterium glutamicum
;  FEATURE:
;  OTHER INFORMATION: ATCC14752
;  NAME/KEY: CDS
;  LOCATION: (398)..(1864)
;  OTHER INFORMATION: thrE gene
US-09-834-721-1

Query Match             96.2%;  Score 1836.0;  DB 9;  Length 2817;
Best Local Similarity   99.0%;  Pred. No. 0;
Matches 1848;  Conservative  0;  Mismatches  19;  Indels  0;  Gaps  0;

Qy      38   CCCCTTTGACCTGCGTGTATTGAGCTGGAAGAAGACTTGAACTTCAACCTACGCATTA   97
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Db      156  CCCCTTTGACCTGCGTGTATTGAGCTGGAAGAAGACTTGAACTTCAACCTACGCATTA   215

Qy      98   CAAGTGCGTTGCCTGCCAATTGCCACTCCAGCACCGCAGATGCTGATGATCAACAAC   157
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Qy   1238  CCGCAGCGGCCTTCGCAGTGGGTTGTTACGGCGGAGTGGTCCTCGGTGATTATTGCGGGGC  1297
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Db   1356  CCGCAGCGGCCTTCGCAGTGGGTTGTTACGGCGGAGTGGTCCTCGGTGATTATTGCGGGGC  1415

Qy   1298  TTACTGCGCTGATGGGTTCTGCGGTTTATTACCTTCGTGTTGTTATTAGGCCCGTCT       1357
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Db   1416  TTACTGCGCTGATGGGTTCTGCGGTTTATTACCTTCGTGTTGTTATTAGGCCCGTCT       1475

Qy   1358  CTGCCGCGTGCGATTGCTGCAACAGCAGTTGGTTTCACTGGTGTTGCTGCCCGTCGAT     1417
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1476  CTGCCGCGTGCGATTGCTGCAACAGCAGTTGGTTTCACTGGTGTTGCTGCCCGTCGAT     1535

Qy   1418  TCTTGATTCCACCGTGATTGTGGCGATTGCCCGGCATCACACCAATGCTTCCAGGTCTAG    1477
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Db   1536  TCTTGATTCCACCGTGATTGTGGCGATTGCCCGGCATCACACCAATGCTTCCAGGTCTAG    1595

Qy   1478  CAATTACCGCGGAATGTACGGCCACCCTGAATGATCAAACACTCATGGGTTTCACCAACA    1537
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Db   1596  CAATTACCGCGGAATGTACGGCCACCCTGAATGATCAAACACTCATGGGTTTCACCAACA    1655

Qy   1538  TTGCGGTTGCTTTAGCCACTGCTTCATCACTTGCCGCGGTGGTTTGGGTGAGTGGA       1597
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Db   1656  TTGCGGTTGCTTTAGCCACTGCTTCATCACTTGCCGCGGTGGTTTGGGTGAGTGGA       1715

Qy   1598  TTGCCCGGCAGGCTACGTCGTCCACCACGCTTCAACCATACCGTCGCATTTACCAAGGCGA   1657
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Db   1716  TTGCCCGGCAGGCTACGTCGTCCACCACGCTTCAACCATACCGTCGCATTTACCAAGGCGA   1775

Qy   1658  ATGAGTTCTCCTTCCAGGAGGAAGCTGAGCAGAATCAGCGCGCCGGCAGAGAAACGTCCAA   1717
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1776  ATGAGTTCTCCTTCCAGGAGGAAGCTGAGCAGAATCAGCGCGCCGGCAGAGAAACGTCCAA   1835

Qy   1718  AGACTAATCAGAGATTCGGTAATAAAGGTAAAAATCAACCTGCTTAGGCGTCTTTCGCT    1777
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Db   1836  AGACTAATCAGAGATTCGGTAATAAAGGTAAAAATCAACCTGCTTAGGCGTCTTTCGCT    1895

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Db   1896  TAAATAGCGTAGAATATCGGGTCGATCGTTTTAAACACTCAGGAGGATCCAGAGGAAACCGCA  1955

Qy   1838  AAAATCACGGACACTCGTCCCACCCCAGAATCCCTTGTTGAAGAGGAAACCGCA         1897
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Db   1956  AAAATCACGGACACTCGTCCCACCCCAGAATCCCTTCACGCTCTTGAAGAGGAAACCCGCA   2015

Qy   1898  GCCGGGG   1904
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Db   2016  GCCGGTG   2022
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Qy    158  TACGAATACGTATCTTAGCGTATGTGTACATCACAATGGAATTCGGGCTAGTAGAGTATCTG   217
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Db    276  TACGAATACGTATCTTAGCGTATGTGTACATCACAATGGAATTCGGGCTAGTAGAGTATCTG   335

Qy    218  GTGAACCGTGCATAAACGACCTGATTGGACTCTTTTTCCTTGCAAAATGTTTCCAGC      277
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    336  GTGAACCGTGCATAAACGACCTGATTGGACTCTTTTTCCTTGCAAAATGTTTCCAGC      395

Qy    278  GGATGTTGAGTTTTGGACCCCTTCGTCGCCGATTCAACAGTTGACGCTGCAAAAGCCG     337
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    396  GGATGTTGAGTTTTGGACCCCTTCGTCGCCGATTCAACAGTTGACGCTGCAAAAGCCG     455

Qy    338  CACCTCCGCCATCGCCACTAGCCCGATTGATCTCACTGACCATAGTCAAGTGGCCGGTG    397
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    456  CACCTCCGCCATCGCCACTAGCCCGATTGATCTCACTGACCATAGTCAAGTGGCCGGTG    515

Qy    398  TGATGAATTTGGCTGCGGAGAATTGGCGATATTTGCTTTCTTCAGGTACGTCAAATAGTG   457
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Db    516  TGATGAATTTGGCTGCGGAGAATTGGCGATATTTGCTTTCTTCAGGTACGTCAAACAGTG   575

Qy    458  ACACCAAGGTACAAGTTCGAGCAGTAGTGACCTCTGCGTACGGTTTGTACTACACGCACGTGG  517
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Db    576  ATACCAAGGTGCAAGTTCGAGCGGTGACCTCTGCGTATGGCGTATACGCATGTGG       635

Qy    518  ATATCACGTTGAATACGATCACCATCTTCACCAAACATCGGTGTGGAGAGATGCCGG      577
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    636  ATATCACGTTGAATACGATCACCATCTTCACCAAACATCGGTGTGGAGAGATGCCGG      695

Qy    578  TCAACGTGTTTCATGTTGTAGGCAAGTTGGACACCAACTTCTCCAAACTGTCTGAGGTTG    637
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Db    696  TCAACGTGTTTCATGTTGTGGGCAAGTTGGACACCAACTTCTCCAAACTGTCTGAGGTTG    755

Qy    638  ACCGTTTGATCCGTTCCATTCAGGCTGCTGGTGCGCCACCCCGCCCTGAGGTTGCCGAGAAATCC   697
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    756  ACCGTTTGATCCGTTCCATTCAGGCTGCTGGTGCGCCACCCCGCCCTGAGGTTGCCGAGAAATTC   815

Qy    698  TGGACGAGTTGGAGCAATCCCCTGCCGTCTTATGGTTTCCCTGTTGCCGTTGGCTGGG      757
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Db    816  TGGACGAGTTGGAGCAATCCCCTGCCGTCTTATGGTTTCCCTGTTGCCGTTGGCTGGG      875

Qy    758  CAATGATGGGGTGGTGCGCGTGTTCTGCTGTTGGGTGGTGGCAGGTTTCCCTAATTG      817
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    876  CAATGATGGGGTGGTGCGCGTGTTCTGCTGTTGGGTGGTGGCAGGTTTCCCTAATTG      935

Qy    818  CTTTTATTACCCGCGTTCACGATCATTGCCACGACGTCATTTTTGGGAAAGAAAGGGTTTGC   877
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    936  CTTTTATTACCCGCGTTCACGATCATTGCCACGACGTCATTTTTGGGAAAGAAAGGGTTTGC   995

Qy    878  CTACTTCTTCTTCCAAAATGTTGTTGGTGGTTTATTGCCACGCTGCCTGCGATTGCTT     937
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Db    996  CTACTTCTTCTTCCAAAATGTGTTGGTGGTTTATTGCCACGCTGCCTGCGATTGCTT      1055

Qy    938  ATTCTTTGGGCGTGCAATTTGCATTTGCATTTTGCATTTTGTCTTGAGATCAAAACCGAGCCGACGATCATCGGAA  997
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1056  ATTCTTTGGGCGTGCAATTTGCATTTGTCTTGAGATCAAACCGAGCCGACGATCATCGGAA    1115

Qy    998  TTGTTGTCGTGTTGGAGCAATCTCGTGCAATCTCTGCAGACGCCATCACGGGGCG        1057
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Db   1116  TTGTTGTCGTGTTGGAGCAGTTTGCACTTGTGCAATCTCTGCAGACGCCATCACGGGGCG    1175

Qy   1058  CTCCGGTGACAGCAAGTGCACGATTTTTGGAAACACTCCTGTTTACCGGCCATTGTTG     1117
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Db   1176  CTCCGGTGACAGCAAGTGCACGATTTTTGTTTACCGGCGCGCATTGTTG             1235

Qy   1118  CTGGGCGTGGGGTTTGGGCATTCAGCTTTTCAGCTTTCTGAAATCTTGCGATGTCATGTTGCGCTGCCATGG  1177
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1236  CTGGGCGTGGGGTTTGGGCATTCAGCTTTCAGCTTTCTGAAATCTTGCGATGTCATGTTGCGCTGCCATGG    1295

Qy   1178  AGTCCGCTGCGAGCACTAATTATTCGTCTACATTCGCCCGCATTCGGCCCGTGTTGGCGTCA   1237
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1296  AGTCCGCTGCGAGCACTAATTATTCGTCTACATTCGCCCGCATTCGGCCCGTGTTGGCGTCA   1355
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US-09-783-388-1

Query Match   96.2%;   Score 1836.6;   DB 9;   Length 2817;
Best Local Similarity   99.0%;   Pred. No. 0;
Matches 1848;   Conservative   0;   Mismatches   19;   Indels   0;   Gaps   0;

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Qy      38 CCCCTTTGACCTGGTGTTATTGAGCTGGAGAAGACTTGAACTCTCAACCTACGCATTA 97
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Db     156 CCCCTTTGACCTGGTGTTATTGAGCTGGAGAAGACTTGAACTCTCAACCTACGCATTA 215

Qy      98 CAAGTGCGTTGCGCTGCCAATGCGCCACTCCAGCACCGACGATGCTGATGATCAACAAC 157
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Db     216 CAAGTGCGTTGCGCTGCCAATGCGCCACTCCAGCACCGACGATGCTGATGATCAACAAC 275

Qy     158 TACGAATACGTATCTTAGCGTATGTGTACATCACAATGGAATTCGGGGCTAGAGTATCTG 217
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     276 TACGAATACGTATCTTAGCGTATGTGTACATCACAATGGAATTCGGGGCTAGAGTATCTG 335

Qy     218 GTGAACCGTGCATAAACGACCTGTGATTGGACTCTTTTTCCTTGCAAAATGTTTTCCAGC 277
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     336 GTGAACCGTGCATAAACGACCTGTGATTGGACTCTTTTTCCTTGCAAAATGTTTTCCAGC 395

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           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     396 GGATGTTGAGTTTGGCGACCCTTCGTGGCCGCATTTCAACAGTTGACGCTGCAAAGCCG 455

Qy     338 CACCTCCGCCATCGCCACTAGCCCGATTGATCTCACTGACCATAGTCAAGTGGCCGGTG 397
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Db     456 CACCTCCGCCATCGCCACTAGCCCGATTGATCTCACTGACCATAGTCAAGTGGCCGGTG 515

Qy     398 TGATGAATTTGGCTGCGGAGAATTGGCGATATTTGCTTCTTCAGTGACGTCAAATAGTG 457
           ||||||||||||||||||||||||||||||||||||||||||||||||||| |||||
Db     516 TGATGAATTTGGCTGCGGAGAATTGGCGATATTTGCTTCTTCAGGTACGTCAAACAGTG 575

Qy     458 ACACCAAGGTACAAGTTCGAGCAGTCGAGCGGTGACCTCTGCGTTGTACTACACGCACGTGG 517
           ||||||||| ||||||||||| ||||||||||||||||||||| |||||| ||||| |||||
Db     576 ATACCAAGGTGCAAGTTCGAGCGGTGACCTCTGCGTATGGCGTCTGTACTATACGCATGTGG 635

Qy     518 ATATCACGTTGAATACAGATCACCATCTTCACCAACATCGGTGTGTGGAAGATGCGG 577
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     636 ATATCACGTTGAATACAGATCACCATCTTCACCAACATCGGTGTGTGGAAGATGCGG 695

Qy     578 TCAACGTGTTCATGTTGTAGGCAAGTTGGACACCAACTTCTCCAAACTGTCTGAGGTTG 637
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Db     696 TCAACGTGTTCATGTTCATGGCGGTGCAAGTTGGACCAACTTCTCCAAACTGTCTGAGGTTG 755

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Db     756 ACCGGTTTGATCCGTTCCATTCAGGCTGGTGCGGACCCCGCCTGGTTGCCGAGAAAATTC 815

Qy     698 TGGACGAGTTGGAGCAATCCCCTGTGTTTCCCTGTTGCCTTGGTTGCCCTGTTGGCTGGG 757
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Db     816 TGGACGAGTTGGAGCAATCGCCTGCGTCTTATGGTTTCCCTGTTGCCTGTTGGCTGGG 875

Qy     758 CAATGATGGGTGGTGCGGCCGTCGTGTTGCGTGTTGGTGTGGATGGCGCAGGTTTCCCTAATTG 817
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Db     876 CAATGATGGGTGGTGCGGCCGTCGTGTTGCGTGTTGGTGTGGATGGCGCAGGTTTCCCTAATTG 935

Qy     818 CTTTTATTACCGCGTTCACGATCATTGCCACGACGTCATTTTTGGGAAAGAAGGGTTTGC 877
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Qy     878 CTACTTTCTTCCTTCCAAAATGTTGTGGTGGTTTTATTGCCACCGTCGCCTGATTGCTTT 937
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Db     996 CTACTTTCTTCCTTCCAAAATGTTGTGGTTGGTTTTATTGCCACCGTCGCCTGATTGCTTT 1055

Qy     938 ATTCTTTGGCGTTGCAATTTGGTCTTTGAGATCAAACCGAGCCAGATCATCGGCCATCTGGAA 997
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Qy    1478 CAATTTACCGCGGAAATGTACGCCACCCGAATGATCAAACACTCATGGTTTCACCAACA 1537
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Qy    1898 GCCGGGG 1904
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Db    2016 GCCGGTG 2022
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; TITLE OF INVENTION:  USING CORYNEFORM BACTERIA
; FILE REFERENCE: 21123/282415/MAS
; CURRENT APPLICATION NUMBER: US/09/951,535
; CURRENT FILING DATE:  2001-09-14
; PRIOR APPLICATION NUMBER: 09/431,099
; PRIOR FILING DATE:  1999-11-01
; PRIOR APPLICATION NUMBER: DE 199 41 478.5
; PRIOR FILING DATE: 1999-09-01
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
;
US-09-951-535-1
;
; SEQ ID NO 1
; LENGTH: 2817
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (398)..(1864)
; OTHER INFORMATION: thrB-Gen
US-09-951-535-1

Query Match         96.2%;  Score 1836.6;  DB 10;  Length 2817;
Best Local Similarity   99.0%;  Pred. No. 0;
Matches 1848;  Conservative    0;  Mismatches   19;  Indels    0;  Gaps    0;
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Qy       218 GTGAACCGTGCATAAAACGACCTGTGATTGGACTCTTTTCCTTGCAAAATGTTTTCCAGC 277
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Qy       578 TCAACGTGTTCATGTGTGTAGGCAAGTTGGACACCAACTTCTCCAAACTCTCAAACTGTCTGAGGTTG 637
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Qy       638 ACCGTTGATCCGTTCAGGCTGCGCTGCGACCCCGTGCTTCCCTGTTTCCCTGTTTGCCGAGAAAATCC 697
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Qy       758 CAATGATGGGTGGTGCTGTTGTGTCGTGCTGTGCTCGTGTGGGTGGTGGTGATGGCGAGTGGCAGGTTCCCTAATTG 817
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Db       876 CAATGATGGGTGGTGCCGTCTGTTGTGTCGTGCTGCTGTTGGGTGGTGATGGCGAGTGGCAGGTTCCCTAATTG 935

Qy       818 CTTTTATTACGGCCGTTCACGACGTCATTTGGGAAAGAAGGGTTTGC 877
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Db       936 CTTTTATTACGGCCGTTCACGATCATTTGGGAAAGAAGGGTTTGC 995

Qy       878 CTACTTCTTCCAAAATGTTGTTGGTGGTTTATTGCCACGCTCGCTGCCGATTGCTT 937
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Qy       938 ATTCTTTGGGGTTGCAATTGCTTGAGATAATTTTGAGATCAAACCGAGCCAGATCATCGCATCTGGAA 997
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Qy      1058 CTCCGGTGACAGCAAGTGCACGATTTTCGAAACACTCCTGTTACCGGCGGCATTGTTG 1117
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1176 CTCCGGTGACAGCAAGTGCACGATTTTTGAAACACTCCTGTTACCGGCGGCATTGTTG 1235

Qy      1118 CTGGGGTGGGTTGGGCATTCAGCTTTCTCGAAATCTTGCATGTCATGTGCTGCCATGG 1177
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Qy      1178 AGTCCGCTGCAGCACTCAATTATTGTCTACATTCGCCCCGCCATTATCGCTTGGTGCGTGGTCA 1237
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Qy      1238 CCGCAGCGGCCTTCGCAGTGGGTGTTGTACGCGGAGTGGTCCTCGGTGATTATTGCGGGGC 1297
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Qy      1418 TCTTGATTCACCGTTGATTGTGGGCATTGCCGGCGGCATCAAATGATCAAAACTCATGGGTTTCACCAACA 1477
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Db      1896 TAAATAGCTAGAATATCGGGTCGATCGGTTTAAACACTCAGGAGGAGATCCTTGCCGCC 1955

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Db   1956 AAAATCACGGACACTCGTCCCACCCCAGAATCCCTTCACGCGTCGTGTTGAAGAGAGAAACCCGCA 2015

Qy   1898 GCCGGGG 1904
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Db   2016 GCCGGTG 2022
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RESULT 13
US-10-224-574-9
; Sequence 9, Application US/10224574
; Publication No. US20040101837A1
; GENERAL INFORMATION:
; APPLICANT: Forschungszentrum Jlich GmbH; P. Ziegler, L. Eggeling, H. Sahm,
; APPLICANT: P. Peters- Wendisch
; TITLE OF INVENTION: Nukleotide sequences coding for proteins parcipitating in the syn
; TITLE OF INVENTION: L-Serin, improved process for the microbial manufacture of L-ser
; TITLE OF INVENTION: genetically modified microorganism suitable for the process.
; FILE REFERENCE: FZJ-9912-PCT
; CURRENT APPLICATION NUMBER: US/10/224,574
; CURRENT FILING DATE: 2002-08-21
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
;
; SEQ ID NO 9
; LENGTH: 2817
; TYPE: DNA
; ORGANISM: C. glutamicum ATCC 14 752
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (398)..(1867)
; OTHER INFORMATION: thr E (Threonin-exportcarrier)
US-10-224-574-9

Query Match   96.2%; Score 1836.6; DB 17; Length 2817;
Best Local Similarity 99.0%; Pred. No. 0;
Matches 1848; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

Qy   38 CCCCTTTGACCTGGTGTTATTGAGCTGGAAGAAGACTTGAACTCTCAACCTACGCATTA 97
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Qy   98 CAAGTGGCGTTGCGCTGCCAATTGCGCCACTCCAGCACCGCAGATGCTGATGATCAACAAC 157
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Db   816 TGGACGAGTTGGAGCAATCGCCTCGTCGTTATGGTTCCCGTGTTGGTGCTTGGCTGGG 875

Qy   758 CAATGATGGGTGGTGCGCTGTGCTGTCGTGTGGTGGTGGTGGATGGCAGGTTTCCCTAATTG 817
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Db  1236 CTGGCGTGGGTTTGGGCATTCAGCTTTCTGAAATCTTCGAAAATCTTGCATGTCATGTTGCCTGCCATGG 1295

Qy  1178 AGTCCGCTGCAGCACCGGTTGGTTCCTACTGGTCGTCCGTGGTGTGGTCCGGTCA 1237
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1296 AGTCCGCTGCAGCACCGGTTGGTTCCTACTGGTCGTCCGTGGTGTGGTCCGGTCA 1355

Qy  1238 CCGGCAGCGGCCTTCGCAGTGGTTGTTACGCGGAGTGGTCCTCGGCGTGATTATTGCGGGGC 1297
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1356 CCGCAGCGGCCTTCGCAGTGGTTGTTACGCGGAGTGGTCCTCGGCGTGATTATTGCGGGGC 1415

Qy  1298 TTACTGCGATGGTTCTCGCGTTTATTACCTCTCGTGTTATTTAGGCCCCGTCT 1357
         |||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1416 TTACTGCGATGGTTCTCGCGTTTATTACCTCTCGTGTTATTTAGGCCCCGTCT 1475

Qy  1358 CTGCCGCTGCGATTGCTGCAACAGCAGTTGGTTCACTCGGTTGCTTGCCCGTCGAT 1417
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1476 CTGCCGCTGCGATTGCTGCAACAGCAGTTGGTTCACTCGGTTGCTTGCCCGTCGAT 1535

Qy  1418 TCTTGATTCCACCGTTGATTGTCGGCGATTGCCGGCATCACCATCAACAATGCTTCCAGGTCTAG 1477
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1536 TCTTGATTCCACCGTTGATTGTGCGGATTGCCGGCATCACCATCAACAATGCTTCCAGGTCTAG 1595

Qy  1478 CAATTTACCGCGGAATGATACGCCACCCTGAATGATCAAACACTCATGGGTTCACCAACA 1537
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1596 CAATTTACCGCGGAATGATACGCCACCTTGAATGATCAAACACTCATGGGTTTCACCAACA 1655

Qy  1538 TTGCGGTTGCTTTAGCCACTGCTTCATCGCCGCTGGCGTGGTTTTGGGGTGAGTGGA 1597
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1656 TTGCGGTTGCTTTAGCCACTGCTTCATCGCCGCTGGCGTGGTTTTGGGGTGAGTGGA 1715

Qy  1598 TTGCCCGAGGCTACGTCGTCACCACGGTCAACCCATACCGTGCATTTACCAAGGCGA 1657
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1716 TTGCCCGAGGCTACGTCGTCCACCACGGTCAACCCATACCGTGCATTTACCAAGGCGA 1775

Qy  1658 ATGAGTTTCCTTCCAGGAGGAAGCTGAGCAGAATCAGCGCCGCAGAGAACGTCCAA 1717
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db    1776  ATGAGTTCTCCTTCCAGGAGGAAGCTGAGCGAATCAGCGCCGCGAGAGAAAAGTCCAA  1835

Qy    1718  AGACTAATCAGAGATTCGGTAATAAAAGGTAAAAATCAACCTGCTTGCTTTCGCT  1777
            ||||||  |||||  ||||||||||||||||||||||||||||||||||| ||||||
Db    1836  AGACTAATCAAAGATTCGGTAATAAAAGGTAATAAAATCAACCTGCTTTAGGCGTCTTTCGCT  1895

Qy    1778  TAAATAGCGTAGAATATCGGGTCGATCGCTTTAAACACTTCAGGAGGATCCTTGCCGGCC  1837
            ||||||||||||||||||||||||| |||||||||||||||||||||||||||||||||
Db    1896  TAAATAGCGTAGAATATCGGGTCGATCGCTTTAAACACTTCAGGAGGATCCTTGCCGGCC  1955

Qy    1838  AAAATCACGGACACTCGTCCCACCCCAGAATCCCTTCACGCTGTTGAAGAGGAAACCGCA  1897
            ||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db    1956  AAAATCACGGACACTCGTCCCACCCCCAGAATCCCTTCACGCTGTTGAAGAGGAAACCGCA  2015

Qy    1898  GCCGGGG  1904
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Db    2016  GCCGGTG  2022
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RESULT 14
US-10-627-476-557

; Sequence 557, Application US/10627476
; Publication No. US20040030116A1
; GENERAL INFORMATION:
;  APPLICANT: Pompejus, Mark
;  APPLICANT: Kroger, Burkhard
;  APPLICANT: Schoder, Hartwig
;  APPLICANT: Zelder, Oskar
;  APPLICANT: Haberhauer, Gregor
;  TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS
;  TITLE OF INVENTION: INVOLVED IN MEMBRANE SYNTHESIS AND MEMBRANE
;  TITLE OF INVENTION: TRANSPORT
;  FILE REFERENCE: BGI-125CPCN
;  CURRENT APPLICATION NUMBER: US/10/627,476
;  CURRENT FILING DATE:  2003-07-25
;  PRIOR APPLICATION NUMBER: 09/602,787
;  PRIOR FILING DATE: 2000-06-23
;  PRIOR APPLICATION NUMBER: USSN 60/141031
;  PRIOR FILING DATE: 1999-06-25
;  PRIOR APPLICATION NUMBER: DE 19931454.3
;  PRIOR FILING DATE: 1999-07-08
;  PRIOR APPLICATION NUMBER: DE 19931478.0
;  PRIOR FILING DATE: 1999-07-08
;  PRIOR APPLICATION NUMBER: DE 19931563.9
;  PRIOR FILING DATE: 1999-07-08
;  PRIOR APPLICATION NUMBER: DE 19932122.1
;  PRIOR FILING DATE: 1999-07-09
;  PRIOR APPLICATION NUMBER: DE 19932124.8
;  PRIOR FILING DATE: 1999-07-09
;  PRIOR APPLICATION NUMBER: DE 19932125.6
;  PRIOR FILING DATE: 1999-07-09
;  PRIOR APPLICATION NUMBER: DE 19932128.0
;  PRIOR FILING DATE: 1999-07-09
;  PRIOR APPLICATION NUMBER: DE 19932180.9
;  PRIOR FILING DATE: 1999-07-09
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 678
;
; SEQ ID NO 557
;  LENGTH: 1590
;  TYPE: DNA
;  ORGANISM: Corynebacterium glutamicum
;  FEATURE:
;  NAME/KEY: CDS
;  LOCATION: (101)..(1567)
;  OTHER INFORMATION: RXN00349
US-10-627-476-557

Query Match          83.3%;  Score 1590;  DB 16;  Length 1590;
Best Local Similarity 100.0%;  Pred. No. 0;
Matches 1590;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;
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Qy     180  TGTGTACATCACAATGGAATTCGGGGCTAGAGTATCTGGTGAACCGTGCATAAACGACCT  239
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Db       1  TGTGTACATCACAATGGAATTCGGGGCTAGAGTATCTGGTGAACCGTGCATAAACGACCT  60

Qy     240  GTGATTGGACTCTTTTTCCTTGCAAAATGTTTTCCAGCGGATGTTGAGTTTTGCGACCCT  299
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61  GTGATTGGACTCTTTTTCCTTGCAAAATGTTTTCCAGCGGATGTTGAGTTTTGCGACCCT  120

Qy     300  TCGTGCCGCATTCAACAGTTGACGCTGCAAAGCGCACTCCCGCCATCGCCACTAGC  359
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121  TCGTGCCGCATTCAACAGTTGACGCTGCAAAGCGCACTCCCGCCATCGCCACTAGC  180

Qy     360  CCCGATTGATCTCACTGACCATAGTCAAGTGGCCGGTGTGATGAATTGGCTGCGAGAAT  419
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181  CCCGATTGATCTCACTGACCATAGTCAAGTGGCCGGTGTGATGAATTGGCTGCGAGAAT  240

Qy     420  TGGCCGATATTTGCTTCTTCAGGTACGTACGTCAAAATAGTGACACCAAGGTACAAGTTCGAGC  479
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241  TGGCCGATATTTGCTTCTTCAGGTACGTACGTCAAAATAGTGACACCAAGGTACAAGTTCGAGC  300

Qy     480  AGTGACCTCTGCGTACGGTTGTACTACACGCACGTGGATATCACGTTGAATACGATCAC  539
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301  AGTGACCTCTGCGTACGGTTGTACTACACGCACGTGGATATCACGTTGAATACGATCAC  360

Qy     540  CATCTTCACCAACATCGGTGTGGAGAGGAAGATGCCGGTCAACGTGTTTCATGTTGTAGG  599
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361  CATCTTCACCAACATCGGTGTGGAGAGGAAGATGCCGGTCAACGTGTTTCATGTTGTAGG  420

Qy     600  CAAGTTGGACACCAACTTCTCCAAACTGTCTGAGGTTGACCGTTGATCCGTTCCATTCA  659
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421  CAAGTTGGACACCAACTTCTCCAAACTGTCTGAGGTTGACCGTTGATCCGTTCCATTCA  480

Qy     660  GGCTGGTGCGACCCCCCTGAGGTTGCCGAGAAATCCTGACGAGTTGGAGCAATCCCC  719
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     481  GGCTGGTGCGACCCCCCTGAGGTTGCCGAGAAATCCTGACGAGTTGGAGCAATCCCC  540

Qy     720  TGCGTCTTATGGTTTCCCTGTTGCGTTGGCTGGGCAATGATGGGTGGTGCTGTTGC  779
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     541  TGCGTCTTATGGTTTCCCTGTTGCGTTGGCTGGGCAATGATGGGTGGTGCTGTTGC  600

Qy     780  TGTGCGTTGGGTGGTGGATGGCAGGTTTCCCTAATTGCTTTTATTACCGGGTTCACGAT  839
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     601  TGTGCGTTGGGTGGTGGATGGCAGGTTTCCCTAATTGCTTTTATTACCGGGTTCACGAT  660

Qy     840  CATTGCCACGACGTCATTTTGGAAAGAAGAGGGGTTTGCCTACTTCTTCTTCCAAAATGTGT  899
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     661  CATTGCCACGACGTCATTTTGGAAAGAAGAGGGGTTTGCCTACTTCTTCTTCCAAAATGTGT  720

Qy     900  TGGTGGTTTATTGCCACGCTGCCTGCATCGATTGCTTATTCTTGGCGTTGCAATTGG  959
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     721  TGGTGGTTTATTGCCACGCTGCCTGCATCGATTGCTTATTCTTGGCGTTGCAATTGG  780

Qy     960  TCTTGAGATCAAACCGAGCCAGATCATCGCATCTGGAATTGTGTGCTGCTGGCAGGTTT  1019
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     781  TCTTGAGATCAAACCGAGCCAGATCATCGCATCTGGAATTGTGTGCTGCTGGCAGGTTT  840

Qy    1020  GACACTCGTGCAATCTCGCAGGACGGCATCACGGGCGCTCCGGTGACAGCAGTGCACG  1079
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     841  GACACTCGTGCAATCTCGCAGGACGGCATCACGGGCGCTCCGGTGACAGCAGTGCACG  900

Qy    1080  ATTTTTCGAAACACTCCTGTTTACCGGCGGCATTGTTGCTGCGGTTTGGGCATTCA  1139
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     901  ATTTTTCGAAACACTCCTGTTTACCGGCGGCATTGTTGCTGCGGTTTGGGCATTCA  960

Qy    1140  GCTTTCTGAAATCTTGCATGTCATGTTGCCTGCCATCGAGTCCGCAGCACCTAATTA  1199
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     961  GCTTTCTGAAATCTTGCATGTCATGTTGCCTGCCATCGAGTCCGCAGCACCTAATTA  1020

Qy    1200  TTCGTCTACATTCGCCCGCATTATCGGCTGGTTGGCGTCACCGGCGTCACCGGCCTTCGCAGTGGG  1259
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1021  TTCGTCTACATTCGCCCGCATTATCGGCTGGTTGGCGTCACCGGCGTCACCGGCCTTCGCAGTGGG  1080

Qy    1260  TTGGTTACGGCGGAGTGGTCCTCGGTGATTAATTGCGGGGGCTTACTGCGCTGATGGGTTCTGC  1319
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1081  TTGGTTACGGCGGAGTGGTCCTCGGTGATTAATTGCGGGGGCTTACTGCGCTGATGGGTTCTGC  1140
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RESULT 15
US-10-450-055-41
; Sequence 41, Application US/10450055
; Publication No. US20040043953A1
; GENERAL INFORMATION:
; APPLICANT: BASF Aktiengesellschaft
; TITLE OF INVENTION: No. US2004043953A1el genes of Corynebacterium
; FILE REFERENCE: 936_2000
; CURRENT APPLICATION_NUMBER: US/10/450,055
; CURRENT FILING DATE: 2003-06-10
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn Vers. 2.0
; SEQ ID NO 41
; LENGTH: 1590
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (101)..(1567)
; OTHER INFORMATION: RXS00349
US-10-450-055-41

Query Match   83.3%;   Score 1590;   DB 16;   Length 1590;
Best Local Similarity 100.0%;   Pred. No. 0;
Matches 1590;   Conservative 0;   Mismatches 0;   Indels 0;   Gaps 0;

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Db    1261 GGCGATTGCCGGCATCACACCAATGCTTCCAGGTCTCAGCAATTTACCGCGAATGTACGC 1320

Qy    1500 CACCCTGAATGATCAAACACTCATGGGTTTCACCAACATTGCGGTTGCTTTAGCCACTGC 1559
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1321 CACCCTGAATGATCAAACACTCATGGGTTTCACCAACATTGCGGTTGCTTTAGCCACTGC 1380

Qy    1560 TTCATCACTTGCGCGCTGGCGTGGTTTTGGGTGAGTGGATTGCCCGCAGGCTACGTCGTCC 1619
           ||||||||||||||||||||||||||||||||| |||||||
Db    1381 TTCATCACTTGCGCGCTGGCGTGGTTTTGGGTGAGTGGATTGCCCGCAGGCTACGTCGTCC 1440

Qy    1620 ACCACGCTTCAACCCATACCGTGCATTTACCAAGGCGAATGAGTTCTCCTTCCAGGAGGA 1679
           |||||||||||||||||||||||||||||||||||||||||||||||
Db    1441 ACCACGCTTCAACCCATACCGTGCATTTACCAAGGCGAATGAGTTCTCCTTCCAGGAGGA 1500

Qy    1680 AGCTGAGCAGAATCAGCGCCGGCAGAGAAAACGTCCAAAGACTAATCAGAGATTCCGGTAA 1739
           |||||||||||||||||||||||||||||||||||||||||||||||
Db    1501 AGCTGAGCAGAATCAGCGCCGGCAGAGAAAACGTCCAAAGACTAATCAGAGATTCCGGTAA 1560

Qy    1740 TAAAAGTAAAAATCAACCTGCTTAGGCGT 1769
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Db    1561 TAAAAGTAAAAATCAACCTGCTTAGGCGT 1590
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Search completed: January 14, 2005, 15:31:05
Job time : 1012.85 secs